

Db 379 AGCAGCGTGAAGAGGAGGGCCCAAGCACCTCTTGATCTCTGGAGTCTTGTTCGGAGCA 438
Qy 301 GUCAUACGAAGAAGUGUGCGGACCCUGUGGCUUCCUGUGUGUGAAGUACCGCGCGCG 360
Db 439 GTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTCTGTCTCTCAATATCGAGCCAGG 498
Qy 361 GAGCGGUCACGAGGCGGAGUACUGGAGGAGCGUACUACAGACUACAGCUGUUC 420
Db 499 GAGCAGTCAAAAGGAGGAGGAGTCTGAGAGTCTCAAAAATTACAAGCACTGTTTT 558
Qy 421 CCGGAGAUUUUGGCAAGGCGAGCGAGAGCCUGGAGGUGUUCGCAUCCGAGCUCAAG 480
Db 559 CTTGAGATCTTCGCAAGCTCTGAGTCTTGAGTCTTGAGTCTTGAGTCTTGAGTCTG 618
Qy 481 GAGCGGACCGGACCGGCGACGACUACGUGUGUGUACGUGGCGGCGGCGGCGGCGG 540
Db 619 GAAGCAGACCCACCGGCGACTCTATGTCCTGACCTGACCTGAGTCTCTCTATGAT 678
Qy 541 GCGCUGUGGCGGCAACCAAGUACGUGGCGGAGGAGGCGGCGGCGGCGGCGGCGG 600
Db 679 GGCCTGCTGGGTGATATCATAGATCATGCCCAAGACAGGCTTCTGATTAATTGTCCTG 738
Qy 601 AUGAUCGGAUGAGGCGGCGGCGGCGGAGGAGGAGUACUGGAGGAGGAGGAGGAGG 660
Db 739 ATGATTCGATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 798
Qy 661 AUGAGGUCUACGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
Db 799 ATGAGGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 858
Qy 721 CAGGACUUGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
Db 859 CAAGATTTGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 918
Qy 781 CGCUACGAGUUCUGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
Db 919 CGCTATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 978
Qy 841 GAGUACGUCUACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
Db 979 GAGTATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1038

RESULT 2
US-09-949-016-703
; Sequence 703, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 703
; LENGTH: 1624
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-703
Query Match 64.1%; Score 601.6; DB 3; Length 1624;

Best Local Similarity 64.7%; Pred. No. 2.8e-85;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;
Qy 1 AUGAGCCUGGAGCAGCGCAGCCUGUACUGCAAGCCGAGAGGCGUGGAGGCGCAGCAG 60
Db 139 ATGCTCTTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAAA 198
Qy 61 GAGCGCGUGGCGUGGUGUGGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Db 199 GAGCGCGTGGGCGTGGTGTGTCAGAGGCTGCACTCTCTCTCTCTCTCTCTCTCTCT 258
Qy 121 GGCACGCGGAGGAGGUGCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
Db 259 GGCACCTTGAGAGGAGGTCCTGCTGGGTCAACAGATCTCTCCAGAGTCTCTCAGGA 318
Qy 181 GCGAGCGGUGUCCGCGAGCAUACUUCACGCGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 319 GCCTCGGCTTCCCACTACATCACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 378
Qy 241 AGCAGCGCGGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db 379 AGCAGCGTGAAGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 438
Qy 301 GUCAUACGAAGAAGUGUGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
Db 439 GTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTCTGTCTCTCAATATCGAGCCAG 498
Qy 361 GAGCGGUCACGAAGGCGGAGUUGUGGAGAGCGUACUACGAAGAAUACAAAGCAGCUG 420
Db 499 GAGCCAGTCAAAAGGCGAGAAATGCTGGAGAGTGTATCAAAAATTAACAAGCACTG 558
Qy 421 CCGGAGAUUUUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
Db 559 CTTGAGATCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 618
Qy 481 GAGCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
Db 619 GAAGAGACCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 678
Qy 541 GCGCUGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
Db 679 GGCCTGCTGGGTGATATCATAGATCATGCCCAAGAGGCTTCTCTGATTAATTGTCCTG 738
Qy 601 AUGAUCGGAUGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
Db 739 ATGATTCGATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 798
Qy 661 AUGGAGGUCUACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
Db 799 ATGAGAGTGTATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 858
Qy 721 CAGGACCCUGGCGGAGGAGUACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
Db 859 CAAGATTTGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 918
Qy 781 CGCUACGAGUUCUGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
Db 919 CGCTATGAGTCTTGGTGGGCTCAAGGGCCCTCGCTGAACCACTATGTGAAGTCTT 978
Qy 841 GAGUACGUCUACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
Db 979 GAGTATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 936
Qy 901 GCGCUGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 936
Db 1039 GCTTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1074

RESULT 3
US-09-949-016-2688
; Sequence 2688, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2688
; LENGTH: 1624
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-2688

Query Match      64.1%; Score 601.6; DB 3; Length 1624;
Best Local Similarity 64.7%; Pred. No. 2.8e-85;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;

Qy 1 AUGAGCCUGGAGCAGCGCAGCCUGCAGCUCGCAAGCCGAGGAGGCGCGUGGAGCGCAGCAG 60
Db 139 ATGTCCTTTGAGCAGAGAGGTCCTCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 198
Qy 61 GAGCGCGUGGCGUGGUGUGUGCAGCGCGCGAGCAGCAGCAGCAGCAGCCCGUGGUCUG 120
Db 199 GAGCGCCCTGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 258
Qy 121 GGCACGCGUGGAGGAGGCGCGCAGCGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180
Db 259 GGCACCTTGGAGAGGTCGCCACTGCTGGGTCAACAGATCTCTCCAGAGTCCTCAGGGA 318
Qy 181 GCGAGCGGUGUCCGACGAGCAUCAACUUCACGCGCCAGCGCCAGCGAGCGGCGAGC 240
Db 319 GCCTCGCGCTTCCACTACCTACCTCACTTCACTCGACAGAGGCAACCCAGTGGGTTC 378
Qy 241 AGCAGCGCGAGGAGGAGGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 300
Db 379 AGCAGCGGTGAAGAGGAGGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 438
Qy 301 GUCAUCACGAGAGGAGGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 360
Db 439 GTAATCACTAAGAGAGGTCGCTGATTTGGTGTGTTCTGCTCTCTCAATATCAGAGCAG 498
Qy 361 GAGCGGUCACGAGGCGGAGUGCUGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420
Db 499 GAGCGAGTCACAGAGGAGGAGAAATGCTGAGAGTGTCTCAAAATTAACAGCACTGTTT 558
Qy 421 CCGGAGAUUUCGCAAGAGGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 480
Db 559 CCGGAGATCTTCGCAAGAGCCTCTGAGTCTCTGAGCAGCAGCAGCAGCAGCAGCAGCAG 618
Qy 481 GAGCGGAGCAGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 540
Db 619 GAAGCAGACCCACCGGCACTCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 678
Qy 541 GCGCUGUGGCGCAACCAAGAUCCGAGCAGCGGCGUGCUGCUGCUGCUGCUGCUGCUGCUG 600
Db 679 GGCCTGCTGGTGATATCAGATCATGCCCAGACAGAGCTTCTGATTAATGTCCTGCTC 738
Qy 601 AUGAUCGGAUGAGGAGGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 660
Db 739 ATGATTGCAATGAGAGGCGCGCATGCTCTCTGAGGAGGAGAAATCTGGGAGGAGCTGAGTGT 798
Qy 661 AUGAGGUCUACGAGCGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 720
Db 799 ATGAGGAGTGTATGAGGAGGAGCAGCAGTGCCTATGGGAGCCAGGAAGCTGCTCACC 858
Qy 721 CAGGACCCUGGUCAGGAGAGUACUUGGAGUACCGCGCAGGUGCCGAGCAGCAGCAGCAG 780

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2688
; LENGTH: 1624
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-2688

Query Match      64.1%; Score 601.6; DB 2; Length 1691;
Best Local Similarity 64.7%; Pred. No. 2.8e-85;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;

Qy 1 AUGAGCCUGGAGCAGCGCAGCCUGCAGCUCGCAAGCCGAGGAGGCGCGUGGAGCGCAGCAG 60
Db 204 ATGTCCTTTGAGCAGAGGAGTCTGCACTCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263
Qy 61 GAGCGCGUGGCGUGGUGUGUGCAGCGCGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 120
Db 264 GAGCGCCCTGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 323
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Qy 121 GGCACGCGUGAGGAGGUCGCGAGCGGGGCGAGCGGACCGCGCGAGAGCCCGCAGGC 180
Db 324 GGCACCCCTGGAGGAGGTGCCACCTGCTGGGTCAACAGATCCTCCCGAGAGTCTCTCAGGA 383
Qy 181 GCGAGCGGUUCCGAGGAGCAUACAUCACGCGCCAGCGCCAGCGAGCGAGGCGAGC 240
Db 384 GCCTCCGCCCTTCCCATACCATCACTTCACTCGACAGAGCAACCCAGTGAGGGTTCC 443
Qy 241 AGCAGCGCGAGGAGGAGGCGCGAGCAGCGAGCGUCCUGGAGAGCCUGUUCGCGCG 300
Db 444 AGCAGCGGTGAGAGGAGGCGCGAGCAGCCTTGTATCTCTGAGTCTCTGTTCCGAGCA 503
Qy 301 GUCAUACGAAAGGUGCGGAGCCUGGUGCGGUUCCUGUGUGUGAAGUACCGCGCGCG 360
Db 504 GTAATCACTAAGAGGTGGGTGATTTGGTTGGTTCTCTCTCTCAAAATATCAGCGCAGG 563
Qy 361 GAGCGGUGACGAGGCGGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 420
Db 564 GAGCGAGTCAAAAGGAGGAGGAGTCTGAGAGTGTCAAAAATTAAGCACTGTCTTT 623
Qy 421 CCGGAGAUUUCGCGAAGGCGGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 480
Db 624 CCGGAGATCTCGCGAAGGCGGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 683
Qy 481 GAGCGGAGCGGAGGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 540
Db 684 GAAGCAGACCCACCGGCGCATCTCTATGCTCTGCTACCTGCTCTCTCTCTCTCTATGAT 743
Qy 541 GCGGUGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 600
Db 744 GCGCTGCTGGGTGATATCAGATCATGCCCAAGACAGGCTCTCTGATTAATGTCCTGTC 803
Qy 601 AUGAUCGAGGAGGAGGCGGCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
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Qy 661 AUGAGGUGUACGAGCGGCGGAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Db 864 ATGAGGAGTATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 923
Qy 721 CAGGACGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 924 CAAGATTGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 983
Qy 781 CGCUACGAGUUCUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 984 CGCTATGAGTTCTGTGGGTCCAGGGCCCTCGCTGAAACAGCTATGTGAAAGTCTTT 1043
Qy 841 GAGUACGUCUACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
Db 1044 GAGTATGATGATCAAGGTCAAGTCAAGAGTTCGCTTTTCTTCTCCATCCTCGTGAAGCA 1103
Qy 901 GCGUGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 936
Db 1104 GCTTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1139
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RESULT 5

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US-08-845-528C-8
; Sequence 8, Application US/08845528C
; Patent No. 6027924
; GENERAL INFORMATION:
; APPLICANT: LUCAS, Sophie;
; APPLICANT: DE SMET, Charles;
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR
; TITLE OF INVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
```

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; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,528C
; FILING DATE: April 25, 1997
; CLASSIFICATION: 4335
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary Anne Schofield
; REGISTRATION NUMBER: 36,669
; REFERENCE/DOCKET NUMBER: LUD 5455
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1691 base pairs
; TYPE: nucleotides
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; US-08-845-528C-8
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Query Match 64.1%; Score 601.6; DB 3; Length 1691;
Best Local Similarity 64.7%; Pred. No. 2.8e-85;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;

Qy 1 AUGAGCGUGAGGAGGAGCGGCGGAGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
Db 204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCCTGAGGAGGAGGAGGAGGAGGAGG 263
Qy 61 GAGCGCGUGGCGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUG 120
Db 264 GAGCGCGCTGGGCGCTGGTGTGTGAGGCTGCGACCTCTCTCTCTCTCTCTCTCTCTCT 323
Qy 121 GGACGCGUGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db 324 GGCACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 383
Qy 181 GCGAGCGGUGUCCGAGGAGCAUACAUCGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 240
Db 384 GCCTCGCGCTTCCCACTACCATCACTTCACTCGACAGAGGAGGAGGAGGAGGAGGAGG 443
Qy 241 AGCAGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Db 444 AGCAGCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 503
Qy 301 GUCAUACGAAAGGUGGCGGAGCGGAGCGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGAG 360
Db 504 GTAATCACTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 563
Qy 361 GAGCGGUGUACGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
Db 564 GAGCGAGTCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 623
Qy 421 CCGGAGAUUUCGCGAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
Db 624 CCGGAGATCTCGCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 683
Qy 481 GAGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
Db 684 GAAGCAGACCCACCGGCGCATCTCTATGCTCTGCTACCTGCTCTCTCTCTCTCTATGAT 743
Qy 541 GCGGUGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
Db 744 GCGCTGCTGGGTGATTAATCAGATCATGCCCAAGACAGGCTCTCTGATTAATGTCCTGTC 803
Qy 601 AUGAUCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
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Db 804 ATGATTGCAATGAGGGCGGCATGCTCTGAGGAGGAAATCTGGAGGAGCTGAGTGTG 863
Qy 661 AUGGAGGUCAUACGCGCGGACACAGCGGUAACGCGGAGCGCCGACGUCUGACG 720
Db 864 ATGAGGTTGATGATGGAGGAGGACAGTGCCTATGGGAGCCGACGAAAGCTGCTACC 923
Qy 721 CAGGACUUGUCCAGGAGAAAGUACUGGAGUACCGCCAGGUCGCGGACAGCGACCCGGCG 780
Db 924 CAAGATTGGTGCAGGAAAGTACTGGAGTACCGGACAGTGGCGGACAGTATCCCGCA 983
Qy 781 CGUACGAGUUCUGUGGGCCCGCGCGCGCGGCGGCGGAGAGAGAGUACGUAAGGUCUG 840
Db 984 CGCTATGAGTTCTGTGGGTCCAAAGGCCCTCGCTGAACCGAGCTATGTGAAGTCTTT 1043
Qy 841 GAGUACGUCAUACGAGGUCGCGGCGGUCGUCGUCUUCUUCGCGGCGGAGCGG 900
Db 1044 GAGTATGTGATCAAGGTGAGTGCAGAGTTCGCTTTTCCATCCCTCGGTGAAGCA 1103
Qy 901 CGCGUCGCGGAGGAGGAGGCGGCGUCUGAGCGUGA 936
Db 1104 GCTTTGAGAGAGGAGAGAGGAGTCTGAGCATGA 1139

RESULT 6

US-09-066-281B-8
; Sequence 8, Application US/09066281B
; Patent No. 6475783

GENERAL INFORMATION:

; APPLICANT: LUCAS, Sophie; DE SMT, Charles; BOON-FALLEUR, Thierry
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING
; TITLE OF INVENTION: FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGE-C1 AND MAGE-C2
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/066,281B
; FILING DATE: April 24, 1998

CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/845,528
; FILING DATE: April 25, 1997

ATTORNEY/AGENT INFORMATION:

; NAME: Mary Anne Schofield
; REGISTRATION NUMBER: 36,669

; REFERENCE/DOCKET NUMBER: LUD 5455.2 US - JEL/MAS

TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 318-3100
; TELEFAX: (212) 752-5958

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1691 base pairs

; TYPE: nucleotides

; STRANDEDNESS: single stranded

; TOPOLOGY: linear

US-09-066-281B-8

Query Match 64.1%; Score 601.6; DB 3; Length 1691;

Best Local Similarity 64.7%; Pred. No. 2.8e-85;

Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;

Qy 1 AUGAGCCUGGAGCAGCGCAGCGUACUGCAAGCGGAGGCGGCGUGGAGCGCAGAG 60

Db 204 ATGTCTTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263
Qy 61 GAGCGCGUGCGCCUGGUCUGGAGCGGCGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 120
Db 264 GAGCGCGTGGGCTGTGTGTGAGGCTGCGACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 323
Qy 121 GGCACGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db 324 GGCACCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 383
Qy 181 GCGAGCGGCGUUCGCGAGCAGCAUACUACGCGCGCAGCGCCAGCGCCAGCGAGCGGAGC 240
Db 384 GCCTCGCCCTTTCCCACTTACCATCACTTCACTCGACAGAGGCAACCCAGTAGGGTTCC 443
Qy 241 AGCAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
Db 444 AGCAGCGGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 503
Qy 301 GUCAUACAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Db 504 GTAATCACTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 563
Qy 361 GAGCGCGUACAGAAAGCGGAGAGUUGGAGAGCGUACUACAAGAAUACAAGCAGCUGUCU 420
Db 564 GAGCCAGTCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 623
Qy 421 CCGGAGAUUCGCGAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Db 624 CCTGAGATCTTCGCGAAAGCCTCTGAGTCTTGCAGCTGTCTTTGCGATGAGCGTAAG 683
Qy 481 GAGCGGACCCGACGCGGCGCAGCAGCUCGUCGUCGAGCAGGCGGCGGCGGCGGCGGCG 540
Db 684 GAAGCAGACCCACCGGCGCACTCTATGTCCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 743
Qy 541 GGCUGUGGCGGACAAACAGAUACUCCGAAAGCGGCGUUCUUGAUACUUGCUGUCUGUC 600
Db 744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCTGTGATAATTTGCTGCT 803
Qy 601 AUGAUCGAGUAGGCGGCGCCAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db 804 ATGATTGCAATGAGAGGCGGCGCATGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 863
Qy 661 AUGGAGGUCAUACGCGCGCGGAGCAGCAGCGGCGGAGCGCGCGCGCGCGCGCGCGCG 720
Db 864 ATGAGGTGTATGATGGAGGAGCAGTGCCTATGGGAGGCCAGGAGGAGGAGGAGGAGG 923
Qy 721 CAGGACUUGUCCAGGAGAAAGUACUUGGAGUACCGCGCAGGCGCGGAGCAGCGAGCCG 780
Db 924 CAAGATTGGTGCAGGAAAGTACCTGGAGTACCGGCGAGGCGGCGGAGGAGGAGGAGGAG 983
Qy 781 CGCUACGAGUUCUGUGGGCG 840
Db 984 CGCTATGAGTTCTGTGGGTCCAAAGGGCCCTCGCTGAAACCAAGCTATGTGAAGTCTTT 1043
Qy 841 GAGUACGUCAUACAGGUCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Db 1044 GAGTATGTGATCAAGGTGAGTGAAGAGTTCGCTTTTCTTCCATCCCTGCGGTGAAGCA 1103
Qy 901 GCGCUGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 936
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RESULT 7

US-09-468-433C-8

; Sequence 8, Application US/09468433C

; Patent No. 6680191

; GENERAL INFORMATION:

; APPLICANT: LUCAS, Sophie; BOON-FALLEUR, Thierry

; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING FOR

; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-C1

; TITLE OF INVENTION: MAGE-B FAMILIES AND USES THEREOF


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Qy 361 GAGCCGUCACGAGCGGAGAUCCUGGAGGCGUACUAAGACACUAGCUCUC 420
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2574 GAGCCAGTCAAAAGGAGAAATCTGGAGAGTGTATCAAAAATTAAGACACTGT 2633
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 421 CCGGAGAUUUUGGCAAGCGGAGGAGCUCGAGCUCGUGUUCUGGCAUCGACG 480
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Db 2634 CTTGAGATCTTCGCAAGCCTCTGAGTCTTGGAGCTGTCTTGGCATGAGCTG 2693
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 481 GAGCGGACCCGACCGGCGCACGACUACGUCUCCUGGUCAGCUGGCGCUGAGC 540
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Qy 601 AUGAUCGCGAUGGAGGCGCGCACGCGCGGAGGAGGAGUACUGGAGGAGCUC 660
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Db 2814 ATGATTCGATGGAGGCGCGCATCTCTCTGAGGAGGAGATCTGGGAGGAGTG 2873
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Qy 661 AUGGAGGUCUACGACCGCGCGAGCACAGCGCGUACCGCGAGCGCGCAAGCUG 720
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Db 2874 ATGGAGGTGATGATGGAGGAGCACAGTGCCTATGGGAGCCGACGAGTCTC 2933
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Qy 721 CAGGACUGGUCAGGAGGAGUACUUGGAGUACCGCCAGGUCUCCGGACAGGCG 780
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Db 2934 CAAGATTGGTGAGGAGAAAGTACTCTGAGTACCGCGCAGGTGCGGACAGT 2993
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Qy 781 CGCUACGAGUUCUGUGGGCGCGCGCGCGGAGGAGGAGUACUAGGUCUCUG 840
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Db 2994 CGCTATGAGTTCCTGTGGGTCCAAAGGCGCTCGCTGAACCACTATGTGAAG 3053
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 841 GAGUACGUCUACAAAGGUCAGCGCGCGCUGCUGCUGUUCUUCGAGCUCGCG 900
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3054 GAGTATGTGATCAAGGTCAAGTCAAGAGTTCGCTTTTCTCCCATCCCTGCG 3113
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Qy 901 GCGCUGCGCGAGGAGGAGGCGGCGUCUGAGCGUGA 936
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Db 3114 GCTTTGAGAGGAGGAGGAGGAGTCTGAGCATGA 3149
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RESULT 13

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US-07-807-043B-7
; Sequence 7, Application US/07807043B
; Patent No. 5342774
; GENERAL INFORMATION:
; APPLICANT: Boon, Thierry, Van den Eynde, Beno t
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESS: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/807.043B
; FILING DATE: 19911212
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
```

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; FILING DATE: 23-May-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5342774man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 253.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2419 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: singular
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; US-07-807-043B-7
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Query Match 62.8%; Score 589.6; DB 2; Length 2419;
Best Local Similarity 64.6%; Pred. No. 2e-83;
Matches 605; Conservative 121; Mismatches 209; Indels 1; Gaps 1;
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Db 626 ATGTCTCTTGAGCAGAGGAGTCTGCACCTGCAAGCCTTGAGGAGCCCTTGAGG 685
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Qy 61 GAGCGCUGGCGCUGGUCUGGUCAGAGGCGGCGACGAGCAGCAGCAGCCCGCUG 120
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Db 686 GAGGCGCTGGGCGCTGTGTGTGAGGCTGCCACCTCTCTCTCTCTCTCTCTCT 745
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Qy 121 GGCAGCUGGAGGAGGUCGCCGAGCGGCGGCGAGCAGCAGCCCGCAGAGCCCG 180
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Db 746 GGCACCTTGAGGAGGTGCCCACTGTGGTCAACAGATCTCTCCAGAGTCTCTCAG 805
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Qy 181 GCGAGGCGUUCGCCGAGCAGCAUCAAUCUACAGCGCCAGCCAGCGAGCGAGGCG 240
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Db 806 GCCTCCGCTTTCCTCCACTACCATCACTTCACTCGACAGAGGCAACCCAGTAGG 865
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Qy 241 AGCAGCGCGAGGAGGCGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 300
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Db 866 AGCAGCGCTGAAGAGGAGGCGGCAAGCAGCCTCTGTATCTCTGAGTCTTTGTT 925
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Qy 301 GUCAUCACAGAAAGGUCGCGGACCUCCUGCGUCUCCUGCUGUAGUACCGCGCGC 360
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Db 926 GTAATCACTAAGAGGTGGCTGATTTGGTTGTTTCTGCTCTCTCAAAATCAGC 985
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Db 986 GAGCCAGTCAAAAGGCGAGAAATGCTGGAGAGTGTATCAAAAATTAACAAGCA 1045
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Qy 421 CCGGAGAUUUUGGCAAGCGGAGGAGCUCGAGCAGCAGCAGCAGCAGCAGCAG 480
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Db 1046 CTTGAGATCTTCGCGCAAGGCTCTGAGTCTCTGAGTCTCTTGGAGTGTGAG 1105
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 481 GAGCGGACCCGAGCGGCGCACAGCUACGUCUCCUGGUCAGCUGGCGCUGAGC 540
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1106 GAAGCAGACCCACCGGCCACTCTATGTCTTGTCTGCTGCTGCTGCTCTCTAT 1165
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Qy 541 GCGCUGGCGGCGACCAACCAUACUCCGGAAGACGGGCUUCUGAUCAUCGUCUG 600
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1166 GGCCTGCTGGTGTATATCATGATCATGCCCAAGACAGGCTTCTGTGATAATT 1225
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Qy 601 AUGAUCGAGGAGGCGCGCGCAGCGCGGAGGAGGAGUACUUGGAGGAGCUCAG 660
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1226 ATGATTGCAATGGAGGCGCGCATGCTCTCTGAGGAGGAGAAATCTGGGAGG 1285
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Qy 661 AUGGAGGUCUACGAGCGCGCGGAGCAGCGCGUACCGCGGAGCGCGCAAGCUC 720
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1286 ATGGAGGTGATGATGGAGGAGGAGCAGTGCCTATGGGAGGCGCCAGGAGCT 1345
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 721 CAGGACUGGUCAGGAGAAAGUACCGCAGGAGUACCGCAGGUCGCGGACAGCG 780
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1346 CAAGATTGGTGCGGAGAAAGTACCTGGAGTA-CGGCAGGTGCGCGGACAGTGAT 1404
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```


GENERAL INFORMATION:
APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen,
APPLICANT: Lutquin, Christophe; Chomez, Patrick; Traversari, Catia
TITLE OF INVENTION: Tumor Rejection Antigen Precursors Tumor
TITLE OF INVENTION: Rejection Antigens and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,368A
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5925729man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5253.4-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2419 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
PS-08-142-168A-7

Query Match	62.8%	Score 589.6	DB 2	Length 2419
Best Local Similarity	64.6%	Pred. No. 2e+83		
Matches 605	Conservative 121	Mismatches 209	Indels 1	Gaps 1
Qy	1	AUGAGCCUGGAGCGCAGCCUGCAGUCGCAAGCGGAGGCGCUGGAGCGCAGCAG	60	
Db	526	ATGTCTTTGAGCAGAGAGGTCTGCACCTGCAGCCTGAGGAGCCCTTGAGGCCACAA	685	
Qy	61	GAGCGCUGGCGCCUGGUCUGCCAGCGCGCGACGACGACGAGCCGCGUCUCCUG	120	
Db	686	GAGGCCCTTGGGCTTGTTGTGTGAGCGCTGCACCTCTCTCTCTCTCTGTCCTG	745	
Qy	121	GGCAGCGUGGAGGAGGUCCCGACGGCGGAGCAGCGGACCGCGCAGACCGCGAGGC	180	
Db	746	GGCACCTTGGAGGAGGTGCCACATGCTGGGTCAACAGATCTCTCCACAGATCTCAGGGA	805	
Qy	181	GCAGAGCGGUUCCGACGACGAUCAACUUCACGCGCCACGCGCAGCGAGGGCAGC	240	
Db	806	GCCTTCGCGCTTTCCCATACATCAATCTCACTGCAGAGGCAACCCAGTGAGGTTC	865	

Search completed: March 20, 2006, 23:50:33
Job time : 193.385 secs

[illegible]

RESULT 6

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US-10-093-766-41
; Sequence 41, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; APPLICANT: Karof, Adam R.
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
; FILE REFERENCE: PA-0047 US
; CURRENT APPLICATION NUMBER: US/10/093,766
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PERL Program
; SEQ ID NO 41
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030013099A1 410721.1
US-10-093-766-41

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Query Match	64.1%;	Score 601.6;	DB 5;	Length 2420;
Best Local Similarity	64.7%;	Pred. No. 1.2e-135;		
Matches 606;	Conservative 121;	Mismatches 209;	Indels 0;	Gaps 0;

[illegible]

RESULT 7

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US-10-116-802-250
; Sequence 250, Application US/10115802
; Publication No. US20030065157A1
; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US

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Db 1046 CTTGAGATCTTCGCAAGCCTCTGAGTCTTGTGAGCTGTCTTTTGGCATTTGACGTGAAG 1105
Qy 481 GAGCGAGCCGACGGGCCACAGCUACGUCCUGUACUGUCCUGGSCCUGAGCUAGCAC 540
Db 1106 GAAGCAGACCCACCGGCATCTCTATGCTCTTGTCACTGCTCTAGGTCTCTCTATGAT 1165
Qy 541 GGCCTGCTGGGTGATATCAGATCATGCCAAGACAGGCTTCTCTGATATTTGCTCTGCTC 600
Db 1166 GGCCTGCTGGGTGATATCAGATCATGCCAAGACAGGCTTCTCTGATATTTGCTCTGCTC 1225
Qy 601 AUGAUCGGAUGGAGGGGGCCACCGCCGAGAGAGAGAUUCUGGAGGAGCUGAGCUC 660
Db 1226 ATGATTGCAATGAGGGGGCGGCATGCTCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG 1285
Qy 661 AUGGAGGUCAUACAGGCGCGGAGCAGCGCAGCGCUACGCGCGCGCAAGCUCUGACG 720
Db 1286 ATGAGGTGTATGAGGAGGAGCAGTGTCTATGGGAGGCCAGAAAGCTCTCTCACC 1345
Qy 721 CAGGACCUUGGUCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 1346 CAAGATTTGGTGCAAGGAAAGTACCTGGAGTACCGGACAGGTGCGGACAGTGTATCCGCA 1405
Qy 781 GGUACGAGUUCUGUGGGGGCCCGCGCGUGCGGAGAGCAGCUACGUAAGGUCUG 840
Db 1406 CGCTATGAGTTCTGTGGGGTCCAAAGGGCCCTCGCTGAAACCAAGCTATGTGAAAGTCTTT 1465
Qy 841 GAGUACGUCAUACAGGUCAGCGCGCGUGCGCUUCUUCUCCGAGCGCGUGCGGAGCGG 900
Db 1466 GAGTATGTGATCAAGGTGAGTGCAGAGGTTCGCTTTTCCATCCCTGCGTGAAGCA 1525
Qy 901 GCGUGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 936
Db 1526 GCTTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1561

RESULT 9
US-10-741-466-5
; Sequence 5, Application US/10741466
; Publication No. US20040180058A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, M.
; TITLE OF INVENTION: Vaccine Compositions and Methods
; FILE REFERENCE: 25955-003
; CURRENT APPLICATION NUMBER: US/10/741,466
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: 60/435,500
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Influenza A virus
US-10-741-466-5

Query Match 64.1%; Score 601.6; DB 8; Length 2420;
Best Local Similarity 64.7%; Pred. No. 1.2e-135;
Matches 606; Conservative 121; Mismatches 209; Indels 0; Gaps 0;

Qy 1 AUGAGCCUGGAGCAGCGCAGCUGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 60
Db 626 ATGTCTCTTGGAGCAGAGAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 685
Qy 61 GAGCGCUGGCGCUGGUGUCUGCUGCAGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 120
Db 686 GAGGCGCTGGGCGCTGGTGTGTGTCAGGCTGCCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 745
Qy 121 GGCAGCUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db 746 GGCACCTGGAGGAGGTGCCACCTGCTGGGTCAACAGATCTCTCCCGAGAGTCTCTCAGGGA 805
Qy 181 GCGAGCGCGUUCGCCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 240
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Db 806 GCCTCGCCTTTCCCACTTACCTCACTCGACAGAGCAACCACTGAGGGTTC 865
Qy 241 AGCAGCGCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Db 866 AGCAGCGGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 925
Qy 301 GUCAUCAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db 926 GTAACTCACTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 985
Qy 361 GAGCGGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 986 GAGCGAGTCACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1045
Qy 421 CCGGAGAUUCUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Db 1046 CTTGAGATCTTCCGCAAGGCTCTGAGTCTTCTGAGCTCTTCTGAGCTCTTCTGAGCTCTTCTGAG 1105
Qy 481 GAGCGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Db 1106 GAAGCAGACCCACCGGCATCTCTATGCTCTTGTCACTGCTCTAGGTCTCTCTATGAT 1165
Qy 541 GGCCTGCTGGGTGATAATCAGATCATGCCAAGACAGGCTTCTCTGATAATTTGCTCTGCTC 1225
Db 1166 GGCCTGCTGGGTGATAATCAGATCATGCCAAGACAGGCTTCTCTGATAATTTGCTCTGCTC 1225
Qy 601 AUGAUCGGAUGGAGGGGGCCCGCGCGAGCAGCGCGCUACGCGCGAGCGCGCGCAAGCUCUGAGCUC 660
Db 1226 ATGATTGCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1285
Qy 661 AUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Db 1286 ATGAGGTGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1345
Qy 721 CAGGACCUUGGUCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 1346 CAAGATTTGGTGCAAGGAAAGTACCTGGAGTACCGGACAGGTGCGGACAGTGTATCCGCA 1405
Qy 781 GGUACGAGUUCUGUGGGGGCCCGCGCGUGCGGAGAGCAGCUACGUAAGGUCUG 840
Db 1406 CGCTATGAGTTCTGTGGGGTCCAAAGGGCCCTCGCTGAAACCAAGCTATGTGAAAGTCTTT 1465
Qy 841 GAGUACGUCAUACAGGUCAGCGCGCGUGCGCUUCUUCUCCGAGCGCGUGCGGAGCGG 900
Db 1466 GAGTATGTGATCAAGGTGAGTGCAGAGGTTCGCTTTTCCATCCCTGCGTGAAGCA 1525
Qy 901 GCGUGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 936
Db 1526 GCTTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1561

RESULT 10
US-10-657-022-81
; Sequence 81, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANNK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-10-657-022-81

[illegible]

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; Sequence 17, Application US/10807308
; Publication No. US20040241725A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Wenming
; APPLICANT: Dong, Gang
; TITLE OF INVENTION: LUNG CANCER DETECTION
; FILE REFERENCE: 114122-00153
; CURRENT APPLICATION NUMBER: US/10/8-00153
; CURRENT FILING DATE: 2004-03-24
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 17
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-807-308-17

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Query Match	64.1%	Score	601.6	DB	8	Length	2420
Best Local Similarity	64.7%	Pred.	No. 1.2e-135				
Matches	606	Conservative	121	Mismatches	209	Indels	0
Qy	1	AUGAGCUGGAGCAGCGCAGCUGCAGCUGCAGCAGCGCGAGGAGCGCGUGGAGGCGCAGCAG	60				
Db	626	ATGTCTTTGAGCAGAGGAGTCTGCACTGCAAGCCTTGAGGAGCCCTTGAGGCGCCACAA	685				
Qy	61	GAGGCGCUGGGCCUGGUCUGGUCACAGGCGGCGACAGCAGCAGCAGCCCGCUGGUCUG	120				
Db	686	GAGGCGCTGGGCTGGTGTGTGTCAGAGGTGCCACCTCCTCTCTCTCTCTCTCTCTCTG	745				
Qy	121	GGCAGCUGGAGGAGGUCGCGAGCGCGGCGCAGCAGCAGCCCGCGCAGAGCCCGCAGGGC	180				
Db	746	GGCACCTTGGAGAGGTGCCACTGTCTGGGTCAACAGATCCTCCCCAGAGTCTCTCAGGGA	805				
Qy	181	GCAGGCGGUUCCCGACGACGAUCAACUUCACGCGCGCAGCGCCAGCGCAGCGAGGGCAGC	240				
Db	806	GCCTCGCCTTCCCACTACCATCACTTCACTTCGACAGAGGCAACCCAGTAGGAGTTCC	865				
Qy	241	AGCAGCGCGAGGAGGAGGGCCGAGCAGCAGCUGCAUCCUGAGAGACCCUGUUCGGCGG	300				
Db	866	AGCAGCGCTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGAGAGTCTTGTTCGAGCA	925				
Qy	301	GUCAUCACGAAGAAGGUCGCGGACUUGGCGGCUUCUGCUGCUGGAAGUACCGCGCGCGC	360				
Db	926	GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTCTGCTCTCTCAATATCAGACCAGG	985				
Qy	361	GAGCGGCUACGAAAGCGGAGUUGCUGGAGAGCGUCAUCAAGAAACUACAGCAGCUGCU	420				
Db	986	GAGCCAGTCACAAGGCAGAAAATGCTGGAGAGTGTATCAAAAATTAACAGCACTGTTTT	1045				
Qy	421	CGGAGAUUUCGGCAAGGCGAGGAGCCUGCAGCUGGUCUUCGCGCAUCGAGCUACAAG	480				
Db	1046	CCTGAGATCTTCGGCAAAAGCCTCTGAGTCTCTGACGCTGGTCTTTGGCATGACGTGAAG	1105				
Qy	481	GAGCGGACCCGACGGGCCACAGCUACGUCGUGUCAUGGCGCUGGCGCCUGAGCAGCAC	540				
Db	1106	GAAGCAGACCCACCGGCCACTCTATGTCTTGTCTGTCTACCTGCTAGGTCTCTCTATGAT	1165				
Qy	541	GGCUGCUGGGCGACAACCAAGAUCAUCCGGAAGACGGGCUUCUGAUCAUCGUCUCCUG	600				
Db	1166	GGCCTGTGGGTGATATCAGATCATGCCCAAGCAGGCTTCTGTGATAATTTGCTCTGTC	1225				
Qy	601	AUGAUCCGAUGGAGGGCGCCACGCGCGGAGGAGGAGAUUGGAGGAGCUGAGGCGUC	660				
Db	1226	ATGATTTCATGAGGCGCGCCATGCTCTCTGAGAGGAATACTGGGAGGAGCTGAGTGTG	1285				
Qy	661	AUGAGGUCUACGACGGCCCGCAGCAGCGCGGUAACGCGAGCGCGCAAGCUGCUGACG	720				
Db	1286	ATGGAGGTGTATGATGGAGGGAGCAGTGCCTATGGGGAGGCCCAAGGAGCTCTCACC	1345				
Qy	721	CAGAACCUUGCAGGAGAAAGUACCUUGGAGUAACGCCAGGUCUCCGAGCAGCCAGCGGCG	780				
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      AGCAGCGTGAAGAGGGGGGCCAAGCACCTCTTGTATCTCTGGAGTCTCTGTTCGAGCA 925
Qy      301  GUCAUACGAAAGGUCGCGAGCCUGGUCGGUCCUGUGUGAAGUACCGCGCGC 360
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
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      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Qy      361  GAGCCGUCACGAAGGGGAGAGUGGUGAGAGCCUGAUCUACAAGAAUACAAGACUUGCU 420
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Db      986  GAGCCAGTCAAAAGGCGAAGATCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTT 1045
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Qy      421  CCGGAGAUUUCGCAAGGGGAGGAGCCUGAGCCUGAGUGGUCGAGUCGACGUAAG 480
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Db      1046  CCTGAGATCTTCGGCAAGGCTCTGAGTCTCTGAGCTGGTCTTTGGCAITGAGCGTAAG 1105
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Qy      481  GAGCGGACCCGAGCGGCCACAGUAGUCCUGGUCAGUGCCUGGCGCUGAGUACGAC 540
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
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      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Qy      541  GGCUGUGCGGCGCAACACGAGUACUGCCGAAGACGGGCUUCCUGAUCUAGCUGGUC 600
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Db      1166  GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCTCTGATAATTGTCTG 1225
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Qy      601  AUGAUCGAGGAGGGCGGCCACGCGGAGGAGGAGUUCUGGAGGAGCUGAGGUC 660
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
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      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Qy      661  AUGAGGUCUACGACGCGCGGAGCAGCAGCGCUACGCGGAGCGCGCAGCUGCUGACG 720
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Db      1286  ATGGAGGTGATGATGGAGGAGGACAGTGCCTATGGGAGCCAGGAGCTCTCACC 1345
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Qy      721  CAGGACUUGUCCAGGAGAAAGUACUGGAGUACCGCAGUCCCGGACAGCGACCGCG 780
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
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      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Qy      781  CGUACGAGUUCUGUGGGCGCGCGCGGCGGAGAGCAGCAGCAGCAGCAGCAGCUG 840
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Db      1406  CGCTATGAGTTCTGTGGGTCCAAAGGCGCTCGCTGAACACAGCTATGTGAAAGTCT 1465
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Qy      841  GAGUACGUAUACAGGUCAGCGCGCGGCGGUCGUCUUCUCCGAGCGCUGCGGAGCG 900
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Db      1466  GAGTATGTGATCAGGTCAAGTCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAG 1525
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Qy      901  GCGCUGCGCGAGGAGGAGGCGGUCUGAGCGUGA 936
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Db      1526  GCTTTGAGAGAGGAGGAGGAGGAGTCTGAGCATGA 1561
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RESULT 2

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US-11-178-134-6
; Sequence 6, Application US/11178134
; Publication No. US20060019290A1
; GENERAL INFORMATION:
; APPLICANT: University of Pittsburgh - of The Commonwealth System of
; APPLICANT: Higher Education
; APPLICANT: Godfrey, Tony
; APPLICANT: Hughes, Steven
; APPLICANT: Xi, Liqiang
; APPLICANT: Gooding, William E
; APPLICANT: Raja, Siva E
; TITLE OF INVENTION: Identification of Markers in Esophageal Cancer, Colon Cancer,
; FILE REFERENCE: 030160
; CURRENT APPLICATION NUMBER: US/11/178,134
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: 60/586,599
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/587,019
; PRIOR FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 1722
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-178-134-6

Query Match      63.9%; Score 600; DB 12; Length 1722;
Best Local Similarity 64.6%; Pred. No. 6.3e-121;
Matches 605; Conservative 121; Mismatches 210; Indels 0; Gaps 0;

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Db      188  ATGTCTCTTGAGCAGAGGAGTCTGCACCTGCAAGCCTGAGGAAGCCCTTGAGGCCCA 247
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Db      248  GAGGCCCTGGGCTGTGTGTGTGACAGCTGCGCCTCTCTCTCTCTCTCTCTCTG 307
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Qy      121  GGACGCGUGAGGAGGUCGCCGAGCGGGGCGAGCACGAGCCCGCGCAGAGCCCGCAG 180
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
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      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
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Qy      241  AGCAGCGCGAGGAGGGGCGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 300
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Qy      361  GAGCGGUCACGAAGCGGAGAGUUGUGGAGAGCGUACAUAAGAAUACAAGACAC 420
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      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Qy      421  CCGGAGUUCUCCGGAAGCGGAGCGGAGCUCGAGCAGCAGCAGCAGCAGCAGCAG 480
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
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      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Qy      481  GAGCGGACCCGAGCGGCGCACAGCUACGUCUCCUGUACGUGCCUGGCGCUGAG 540
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
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Db      848  ATGGAGGTGTATGATGGGAGGAGCAGATGCCTATATGGGAGCCCGCAAGTCTCAC 907
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Qy      721  CAGGACUUGUCCAGGAGAAAGUACCUUGAGUACCGCCAGGUCUCCGGAAGCGG 780
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Db      908  CAAGATTGTGTGAGGAAAGTACCTGGAGTACCGGCGAGGTGCGGACAGTGTAC 967
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Qy      781  CGCUACGAGUCCUGUGGGCGCGCGCGGCGGAGCAGCAGCAGCAGCAGCAGCAG 840
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Db      968  CGCTATGAGTTCTGTGGGGTCCAAGGGGCCCTTGTCTGAAACCACTATGTGAAAG 1027
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Qy      841  GAGUACGUAUCAAAGGUCAGCGCGCGGCGGUCUCCUGUUCUCCGAGCCUGCGAG 900
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
Db      1028  GAGTATGTGATCAAGGTCAAGTCAAGAGTTCGCTTTTCTTCCCTCCCTGCGTGA 1087
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Qy      901  GCGCUGCGCGAGGAGGAGGAGGCGGUCUUGAGCGUGA 936
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Db      1088  GCTTTGAGAGGAGGAGGAGGAGGAGTCTGAGCATGA 1123
      :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2006, 23:02:13 ; Search time 190.385 Seconds
(without alignment)

8767.110 Million cell updates/sec

Title: US-10-729-830-11

Perfect score: 939

Sequence: 1 augagcugagcgcgcag.....aggcgugagcugacugauga 939

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
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- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	641.6	68.3	1624	3	US-09-392-714-18
2	641.6	68.3	1624	3	US-09-949-016-703
3	641.6	68.3	1624	3	US-09-949-016-2688
4	641.6	68.3	1691	2	US-08-993-118-8
5	641.6	68.3	1691	3	US-08-845-528C-8
6	641.6	68.3	1691	3	US-09-066-281B-8
7	641.6	68.3	1691	3	US-09-468-433C-8
8	641.6	68.3	2420	2	US-08-465-167A-23
9	641.6	68.3	2420	3	US-08-056-105-4
10	641.6	68.3	2420	3	US-08-627-820-23
11	641.6	68.3	5699	3	US-09-949-016-12445
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13	629.6	67.1	2419	2	US-07-807-043B-7
14	629.6	67.1	2419	2	US-08-299-849B-7
15	629.6	67.1	2419	2	US-08-142-368A-7
16	629.6	67.1	2419	3	US-08-967-727-7
17	629.6	67.1	2419	3	US-08-037-230D-7
18	629.6	67.1	2419	3	US-09-583-850-7
19	629.6	67.1	2419	3	US-09-579-197-7
20	629.6	67.1	2419	3	US-09-404-026-7
21	629.6	67.1	2419	3	US-09-312-464-7
22	629.6	67.1	2419	3	US-09-583-848A-7
23	629.6	67.1	5674	2	US-07-807-043B-8
24	629.6	67.1	5674	2	US-08-190-411A-1

25	629.6	67.1	5674	2	US-08-299-849B-8	Sequence 8, Appli
26	629.6	67.1	5674	2	US-08-560-024-1	Sequence 1, Appli
27	629.6	67.1	5674	2	US-08-142-368A-8	Sequence 8, Appli
28	629.6	67.1	5674	3	US-08-967-727-8	Sequence 8, Appli
29	629.6	67.1	5674	3	US-08-037-230D-8	Sequence 8, Appli
30	629.6	67.1	5674	3	US-09-583-850-8	Sequence 8, Appli
31	629.6	67.1	5674	3	US-09-579-197-8	Sequence 8, Appli
32	629.6	67.1	5674	3	US-09-404-026-8	Sequence 8, Appli
33	629.6	67.1	5674	3	US-09-312-464-8	Sequence 8, Appli
34	629.6	67.1	5674	3	US-09-583-848A-8	Sequence 8, Appli
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36	585.6	60.2	1084	2	US-08-458-356-110	Sequence 110, App
37	585.6	60.2	1084	3	US-08-460-736-110	Sequence 110, App
38	585.6	60.2	1084	3	US-09-535-370-110	Sequence 110, App
39	585.6	60.2	1084	3	US-09-663-567-110	Sequence 110, App
40	585.6	60.2	1094	2	US-08-184-009-109	Sequence 109, App
41	585.6	60.2	1094	2	US-08-458-356-109	Sequence 109, App
42	585.6	60.2	1094	3	US-08-460-736-109	Sequence 109, App
43	585.6	60.2	1094	3	US-09-535-370-109	Sequence 109, App
44	585.6	60.2	1094	3	US-09-663-567-109	Sequence 109, App
45	491.6	52.4	1022	3	US-09-056-105-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-392-714-18
; Sequence 18, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tsung
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 1624
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-392-714-18

Query Match	68.3%	Score	641.6	DB	3	Length	1624
Best Local Similarity	67.4%	Pred. No.	6.5e-95				
Matches	631	Conservative	121	Mismatches	184	Indels	0
Qy	1	AUGAGCCUGAGGAGCGCAGCUGCAGCAAGCCGAGGAGCCUGGAGGCCAGAG	60				
Db	139	ATGTCTTTGAGCAGAGGAGTCTGCACTGAGGCTGAGGAGCCCTTGAGGCCACAA	198				
Qy	61	GAGGCCUGGCGCCUGGUGUGUGAGCGCCGCCACACAGCAGCAGCCCGGUGUGUG	120				
Db	199	GAGGCCUGGCGCCUGGUGUGUGAGCGCCGCCACACAGCAGCAGCCCGGUGUGUG	258				
Qy	121	GGCAGCCUGAGGAGGUGCCCGCCGCGGAGCAGCCCGCCAGAGGAGGAGGAGG	180				
Db	259	GGCAGCCUGAGGAGGUGCCCGCCGCGGAGCAGCCCGCCAGAGGAGGAGGAGG	318				
Qy	181	GCCAGCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	240				
Db	319	GCCAGCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	378				
Qy	241	AGCAGCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	300				

Db 379 AGCAGCGTGAAGAGGGGGCCAGCACCTCTGTATCTGGAGTCTTGTTCGGAGCA 438
Qy 301 GUGAUCACCAAGAGGUGGCGGACCCUGGUGGCGUUCUGUGUGUGAUAUACCGGCGCCG 360
Db 439 GTAATCACTAAGAGGTGGCTGATTGTTGGTTTCTGCTCTCAATATCGAGCCAGG 498
Qy 361 GAGCCGUGACCAAGGCGGAGAGUGUGUGAGGUGAGUGAUAUAAGAACUAACAGACACUGUUC 420
Db 499 GAGCCAGTCAAAAGGAGGAGATGCTGAGAGTGTCTATCAAAATTAACAAGCACTGTGTT 558
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Db 559 CTTGAGATCTTCGCAAGGCTCTGAGTCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 618
Qy 481 GAGCCGACCCCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Db 619 GAAGCAGACCCCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 678
Qy 541 GCGGUGUGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
Db 679 GGCCTGCTGGGTGATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 738
Qy 601 AUGAUCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db 739 ATGATTCGAATGGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 798
Qy 661 AUGAGGUGUACGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
Db 799 ATGGAGGTGATGATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 858
Qy 721 CAGGACGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
Db 859 CAAGATTGTGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 918
Qy 781 CGUACGAGUUCUGUGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
Db 919 CGCTATGAGTTCCTGTGGGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 978
Qy 841 GAGUACGUGAUCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Db 979 GAGTATGTGATCAAGGTCAGTGCAGAGAGTTCGCTTTTCTTCCATCCCTGCGTGAAGCA 1038
Qy 901 GCCCUGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 936
Db 1039 GCTTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1074

RESULT 2
US-09-949-016-703
; Sequence 703, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIORITY FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIORITY FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIORITY FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIORITY FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 703
; LENGTH: 1624
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-703
Query Match 68.3%; Score 641.6; DB 3; Length 1624;

Best Local Similarity 67.4%; Pred. No. 6.5e-95;
Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;
Qy 1 AUGAGCCUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
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Qy 61 GAGGCGGUGGCGGUG 120
Db 199 GAGGCGGCTGGGCTGGTGTGTGTCAGGCTGTCCTCTCTCTCTCTCTCTCTCTCTCTCT 258
Qy 121 GGCACCCUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
Db 259 GGCACCCUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 318
Qy 181 GCGAGGCGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
Db 319 GCCTCGGCTTTCCCACTACCATCACTCACTCGACAGAGGCAACCCAGTGAGGGTTC 378
Qy 241 AGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Db 379 AGCAGCGGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 438
Qy 301 GUGAUCACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db 439 GTAACTCACTAAGAGGTGGCTGATTTGGTTGGTTTCTGCTCTCAATATCGAGCCAGG 498
Qy 361 GAGCCGUGAUCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
Db 499 GAGCCAGTCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 558
Qy 421 CCCGAGAUUUCGCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
Db 559 CTTGAGATCTTCGCGCAAGGCTCTGAGTCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTG 618
Qy 481 GAGCCGACCCCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Db 619 GAAGCAGACCCCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 678
Qy 541 GCGGUGUGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
Db 679 GGCCTGCTGGGTGATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 738
Qy 601 AUGAUCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db 739 ATGATTCGAATGGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 798
Qy 661 AUGAGGUGUACGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
Db 799 ATGGAGGTGATGATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 858
Qy 721 CAGGACGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
Db 859 CAAGATTGTGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 918
Qy 781 CGUACGAGUUCUGUGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 919 CGCTATGAGTTCCTGTGGGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 978
Qy 841 GAGUACGUGAUCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Db 979 GAGTATGTGATCAAGGTCAGTGCAGAGAGTTCGCTTTTCTTCCATCCCTGCGTGAAGCA 1038
Qy 901 GCCCUGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 936
Db 1039 GCTTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1074

RESULT 3
US-09-949-016-2688
; Sequence 2688, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:


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Qy 121 GGCACCCUGAGGAGGUGCCACCGCGGCGACGACCGACCCCGCCAGAGCCCGCCAGGGC 180
Db 324 GGCACCCCTGGAGGAGTGGCCACCTGCTGGGTCAACAGATCTCCCGCAGAGTCTCTCAGGA 383
Qy 181 GCCAGCGCCUCCACCAACCAUUAUACCCGCGAGCGCCAGCGCCAGCGGGCAGC 240
Db 384 GCCTCCGCCCTTCCCACTACCATCACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443
Qy 241 AGCAGCCGAGGAGGAGGCGCCAGACACAGCUGCAUCCUGGAGAGCCUGUUCGCGCC 300
Db 444 AGCAGCCGTGAAGAGGAGGCGCCAGACCTTGTATCTCTGGATCTTGTTCGAGCA 503
Qy 301 GUGAUAACCAAGAGGUGCGACCCUGGUGGCGUCCUGUGUGAUAAGUACCGCGCCG 360
Db 504 GTAATCACTAAGAGGTGGCTGATTTGGTGGTTTCTGCTCTCAAAATATCAAGCCAGG 563
Qy 361 GAGCCCGUAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
Db 564 GAGCCAGTCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 623
Qy 421 CCCGAGAUUUCGCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
Db 624 CCTGAGATCTTCGCGAAAGGCTCTGAGTCTTGAGCTGTGCTCAAAATATCAAGCACTGTTT 683
Qy 481 CCCGAGAUUUCGCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
Db 684 GAGCAGACCCACCGGCGACCTCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 743
Qy 541 GGCUGUGGCGGAGCAACCAUAUACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
Db 744 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGAGAGGCTTCTGATAATTTGCTCGTC 803
Qy 601 AUGAUCGCAUGAGGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db 804 ATGATTGCAATGAGGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 863
Qy 661 AUGAGGUGUAACGAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Db 864 ATGAGGAGTGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 923
Qy 721 CAGGACCCUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
Db 924 CAAGATTGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 983
Qy 781 CGCUACGAGUUCUGUGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
Db 984 CGCTATGAGTTCTGTTGGGTCCAAAGGCGCTCGCTGAAACAGCTATGTGAAGTCTCTT 1043
Qy 841 GAGUACGUAUACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
Db 1044 GAGTATGTGATCAAGGTCAGTGCAAGAGTTGCTTTTCTTCCATCCCTCGTGAAGCA 1103
Qy 901 GCCUGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 936
Db 1104 GCTTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1139
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RESULT 5

US-08-845-528C-8

; Sequence 8, Application US/08845528C

; Patent No. 6027924

; GENERAL INFORMATION:

; APPLICANT: LUCAS, Sophie;

; APPLICANT: DE SMET, Charles;

; APPLICANT: BOON-FALLEUR, Thierry

; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR

; TITLE OF INVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch

; STREET: 805 Third Avenue

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; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,528C
; FILING DATE: April 25, 1997
; CLASSIFICATION: 4335
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary Anne Schofield
; REGISTRATION NUMBER: 36,669
; REFERENCE/DOCKET NUMBER: LUD 5455
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1691 base pairs
; TYPE: nucleotides
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; US-08-845-528C-8
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Query Match 68.3%; Score 641.6; DB 3; Length 1691;

Best Local Similarity 67.4%; Pred. No. 6.5e-95;

Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;

Qy 1 AUGAGCCUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60

Db 204 ATGCTCTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 263

Qy 61 GAGGCCCCUGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120

Db 264 GAGGCCCCUGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 323

Qy 121 GGCAACCCUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180

Db 324 GGCAACCCUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 383

Qy 181 GCCAGGCGCUUCCCGCACCAUAUAUACCCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240

Db 384 GCCTCGGCTTTCCCACTACCATCACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC 443

Qy 241 AGCAGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300

Db 444 AGCAGCGCGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 503

Qy 301 GUGAUAACCAAGAGGUGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360

Db 504 GTAATCACTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 563

Qy 361 GAGCCCGUGAGCAAGGCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420

Db 564 GAGCCAGTCAAAAGGCGAGAAATGCTGGAGAGTGTATCAAAAAATTTACAAGCACTGTTT 623

Qy 421 CCCGAGAUUUCGCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480

Db 624 CCTGAGATCTTCGCGAAAGGCTCTGAGTCTCTGAGCTGTGCTTTGGCATTTGAGCTGAAG 683

Qy 481 GAGGCCGACCCCGCCACAGCUACGUGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540

Db 684 GAAGCAGACCCCGCCACCGGCGACTCTATGCTCTTGTACCTGCTAGTGTCTCTCTATGAT 743

Qy 541 GGCUGUGGCGGAGCAACCAUAUAUACCCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600

Db 744 GGCCTGCTGGGTGATAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 803

Qy 601 AUGAUGCCCAUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660

Db 804 ATGATTGCAATGGAGGGCGGCATGCTCTCTGAGGAGGAAATCTGGAGAGCTGAGTGTG 863
Qy 661 AUGGAGGUGUACGAGCGCGGAGGACACAGCGCCUACGCGAGCGCCCGCAACGUGUGUACG 720
Db 864 ATGGAGGTGTATGATGGGAGGGAGGACAGTGCCTATGGGGAGCCCGCAGGAAGCTGCTCACC 923
Qy 721 CAGGACGUGUGCAGGAGGAAGUACCUAGGAGUACCGCCAGGUGCGCGACAGCGACCCCGCC 780
Db 924 CAAGATTTGGTGCAAGAAAGTACCTGGAGTACCGGACAGGTGCGGACAGTGTATCCCGCA 983
Qy 781 GCUACGAGUUCUGUGGGGCGCCCGCGCCUGGCGGAGACCAAGUACGAGUAGGUGUGUG 840
Db 984 CGCTATGAGTTCTCTGGGGTCCAAAGGCGCCCTGCTGAAACCAAGCTATGTGAAAGTCTT 1043
Qy 841 GAGUACGUGAUCAGGUGAGCGCGCGUGGCGUUCUUCUCCAGCGUGCGGAGGCC 900
Db 1044 GAGTATGTGATCAAGGTCAAGTGCAGAGAGTTCGCTTTTCTTCCCATCCCTCGGTGAAGCA 1103
Qy 901 GCCUGCGGAGGAGGAGGGCGUGUGAGCCUGA 936
Db 1104 GCTTTGAGAGAGGAGGAGGAGTCTGAGCATGA 1139

RESULT 6
US-09-066-281B-8
; Sequence 8, Application US/09066281B
; Patent No. 6475783
; GENERAL INFORMATION:
; APPLICANT: LUCAS, Sophie; DE SMET, Charles; BOON-PALLEUR, Thierry
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING
; TITLE OF INVENTION: FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGE-C1 AND MAGE-C2
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/066,281B
; FILING DATE: April 24, 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/845,528
; FILING DATE: April 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary Anne Schofield
; REGISTRATION NUMBER: 36,669
; REFERENCE/DOCKET NUMBER: LUD 5455.2 US - JEL/MAS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3100
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1691 base pairs
; TYPE: nucleotides
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-09-066-281B-8
Query Match 68.3%; Score 641.6; DB 3; Length 1691;
Best Local Similarity 67.4%; Pred. No. 6.5e-95;
Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;
Qy 1 AUGAGCCUGGAGCAGCGAGCGUGGACUGGACUAGCAAGCCCGAGGAGGCCUGGAGGCCGAGCAG 60

Db 204 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 263
Qy 61 GAGGCCUGGGCCUGGUGUGUGGAGGCGCCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 120
Db 264 GAGGCCCTTGGCCCTGGTGTGTGTCAGAGGTGCCACCTCTCTCTCTCTCTCTCTCTCTCT 323
Qy 121 GGCACCCUGGAGGAGGUGCCACCGCGCGAGACACCGCCCGGAGGAGGAGGAGGAGGAGGAG 180
Db 324 GGCACCTTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCTCTCAGGA 383
Qy 181 GCCAGCGCCUUCGCCACCAUCAUCUACCCGCGCAGCGCCAGCCAGCCAGCGAGGCGAGC 240
Db 384 GCCTCCGCTTCTCCCACTACATCACTTCACTCGACAGAGGCAACCCAGTGAAGGTTC 443
Qy 241 AGCAGCGCGAGGAGGAGGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 300
Db 444 AGCAGCGCTGAAGAGGAGGAGGCGCCAAAGCACCTCTGTATCTCTGGAGTCTTGTTCGAGCA 503
Qy 301 GUGAUAACCAAGAGGUGCGCGACCGUGGUGGCUUCUGUGUGUAGUAGUAGUAGUAGUAGUAG 360
Db 504 GTATCACTAAGAGGTGGCTGATTGGTTGGTTTCTGCTCTCTCAATATCGAGCCAGG 563
Qy 361 GAGCCCGUGACCAAGCGCGAGAGUGCGGAGAGCGUGAUAAGAAACUACAAGCACUGCUUC 420
Db 564 GAGCCAGTCAAAAGGCGAGAAATGCTGGAGAGTGTATCAAAATTAACAAGCACTGTTTT 623
Qy 421 CCGGAGAUUUGGCAAGGCGCAGGAGAGCGGUGUGUGUGUGUGUGUGUGUGUGUGUGUG 480
Db 624 CTTGAGATCTTCGCGCAAGGCTCTGAGTCTCTGAGCTGGTCTTTTGGCATTTGAGCTGAAG 683
Qy 481 GAGCGCGACCCACCGCGCACAGCUAGCUGCUGGUGAGCUGCGUGGCGCCUGAGUAGUAGC 540
Db 684 GAAGCAGACCCACCGCGCACTCTGATGTCTTGTGTACCTGCTGCTCTCTCTCTCTCTCT 743
Qy 541 GGCUGUGGCGGACAAACCAAGUACUAGCCCAAGACCGGCUUCCUGAUAUCUGUGUGUGUG 600
Db 744 GGCCTGCTGGGTGATATATCAGATCATGCCCAAGACAGGCTTCTGTGATAATTGTCTCTGTC 803
Qy 601 AUGAUCGCCAUGAGGCGCGCCAGCGCCCGGAGGAGAGAGUAGUAGGAGGAGGAGGAGGAG 660
Db 804 ATGATTGCAATGGAGGCGCGCATGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGT 863
Qy 661 AUGGAGGUGUACGAGCGCGCGAGCAGCAGCGCUACCGCGAGCGCCCGCAACGAGCUGAGC 720
Db 864 ATGGAGGTGTATGATGGGAGGAGCAGTGCCTATGGGAGGCCAGGAGGAGGAGGAGGAGTCT 923
Qy 721 CAGGACCCUGGUGCAGGAGGAAGUACCGGAGUACCGCAGGUGCGCCAGCAGCGACCCCGCC 780
Db 924 CAAGATTTGGTGCAAGAAAGTACCTGGAGTACCGGACAGGTGCGGACAGTGTATCCCGCA 983
Qy 781 CGCUACGAGUUCUGUGGGCGCCCGCGCGCGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 840
Db 984 CGCTATGAGTTCTCTGGGGTCCAAAGGCGCTCGCTGAAAACCAAGCTATGTGAAAGTCTT 1043
Qy 841 GAGUACGUGAUCAGGUGAGCGCGCGUGGCGUUCUUCUCCAGCGUGCGGAGGCC 900
Db 1044 GAGTATGTGATCAAGGTCAAGTGTGCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCA 1103
Qy 901 GCCUGCGCGAGGAGGAGGCGUGUGAGCCUGA 936
Db 1104 GCTTTGAGAGAGGAGGAGGAGTCTGAGCATGA 1139

RESULT 7
US-09-468-433C-8
; Sequence 8, Application US/09468433C
; Patent No. 6680191
; GENERAL INFORMATION:
; APPLICANT: LUCAS, Sophie; BOON-PALLEUR, Thierry
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING FOR
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-C 1
; TITLE OF INVENTION: MAGE-B FAMILIES AND USES THEREOF

[illegible]

Qy	781	CGCUACAGAUUCCUGUGCGGGCCCCCGCCGCGCGGCGAGACCAAGCUAGUGAGGUCCUG	840
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Qy	841	GAGUACGUGAUCAAAGGUGAGCGCCCGCGUGCGCUUUCUCCCCAGCCUUGCGGAGGCC	900
Db	1465	GAGTATGTGATCAAGGTCAAGTCAAGAGTTCGTCTTTTCTTTCCATCCTCGCGTGAAGCA	1524
Qy	901	GCCUCGCGGAGGAGGAGGGCGUGAGGCCUGA	936
Db	1525	GCCTTGAGAGAGGAGGAAGGGAGTCTGAGCATGA	1560

RESULT 14

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US-08-299-849B-7
; Sequence 7, Application US/08299849B
; Patent No. 5612201
; GENERAL INFORMATION:
; APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
; APPLICANT: Leth, Bernard; Szkiora, Jean-Pierre; De Smet, Charles;
; APPLICANT: Chomez, Patrick
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
; TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,849B
; FILING DATE: 1-SEPTEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; APPLICATION NUMBER: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5612201man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5355
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2419 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
US-08-299-849B-7

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RESULT 15

RESULTS IS
US-08-142-368A-7
; Sequence 7, Application US/08142368A
; Patent No. 5925729

Db 901 GCGCUGCGGAGGAGGAGGCGGCGUCUGAGCGUGAUGA 939
US-10-729-830-8
; Sequence 8, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingrid
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; FILE REFERENCE: 2793-1-001PCT/Cip
; CURRENT APPLICATION NUMBER: US/10/729,830
; PRIOR FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 940
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAGE1: wildtype-gene (for comparison)
; FEATURE:
; OTHER INFORMATION: Start codon: atg (nucleotides 5 to 7), stop codon:
; OTHER INFORMATION: tga (nucleotides 932 to 934)
US-10-729-830-8
Query Match 68.3%; Score 641.6; DB 8; Length 940;
Best Local Similarity 67.4%; Pred. No. 8.4e-141;
Matches 631; Conservative 121; Mismatches 184; Indels 0; Gaps 0;
Qy 1 AUGAGCCUGGAGCAGCGCUGCAGCUGCAAGCCGAGGAGGCGCCUGGAGGCCAGCAG 60
Db 5 ATGTCTCTTGAGCAGAGAGGCTGCACCTGCAAGCTGAGGAAGCCCTTGAGGCCCAAA 64
Qy 61 GAGGCCUGGCGCUGGUGUGUGGAGGCCGCGCACAGCAGCAGCAGCAGCAGCAGCAGC 120
Db 65 GAGGCCCTGGGCGCTGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 124
Qy 121 GGCACCCUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
Db 125 GGCACCCUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 184
Qy 181 GCCAGCGCCUCCGCCACCAACCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 240
Db 185 GCTTCGCGCTTCCCACTACCATCACTTCACTCGACAGAGGCAACCAAGTGAAGGTTCC 244
Qy 241 AGCAGCCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
Db 245 AGCAGCCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 304
Qy 301 GUGAUCACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db 305 GTAATCACTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 364
Qy 361 GAGCCCGUGACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
Db 365 GAGCCAGTCACAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 424
Qy 421 CCCGAGAUUUGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Db 425 CCGAGATCTTCGCGAAAGCCCTGAGTCTTGCAGTGTGTCATCAAAATTTACAGCATGTTT 484
Qy 481 GAGCCGAGCCCAACCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 540
Db 485 GAAGCAGACCCCAACCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 544
Qy 541 GGCCUGGCGGAGCAACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600

Db 545 GGCCTGCTGGTGATAATACAGATCATGCCCAAGACAGGCTTCTGTGATAATTGTCTGTGTC 604
Qy 601 AUGAUCGCCAUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db 605 ATGATTGCAATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 664
Qy 661 AUGGAGGUGUACAGACGCGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 720
Db 665 ATGGAGGTGTATGATGGAGGAGGAGCAGTGCCTATGGGAGGCCAGGAGGAGTGTCTCACC 724
Qy 721 CAGGACCCUGGUGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
Db 725 CAAGATTGCTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 784
Qy 781 GGUACAGAUUUCUGUGGGGCG 840
Db 785 CGCTATGAGTTCCTGTGGGGTCCAAAGGGGCGCTCGCTGAAACCACTATGTGAAAAGTCTT 844
Qy 841 GAGUACGUGAUCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Db 845 GAGTATGTGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 904
Qy 901 GCCCUGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 936
Db 905 GCTTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 940
RESULT 4
US-10-085-108-8
; Sequence 8, Application US/10085108
; Publication No. US20020176865A1
; GENERAL INFORMATION:
; APPLICANT: LUCAS, Sophie; BOON-PALLEUR, Thierry
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING
; FOR
; TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-
; B
; MAGE-B FAMILIES AND USES THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/085,108
FILING DATE: 01-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/501,104
FILING DATE: 09-Feb-2000
APPLICATION NUMBER: 09/468,433
FILING DATE: December 17, 1999
APPLICATION NUMBER: 09/066,281
FILING DATE: April 24, 1998
APPLICATION NUMBER: 08/845,528
FILING DATE: April 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5611.1 JEL/WAS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3100
TELEFAX: (212) 318-3400
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

Db 1346 CAAGATTTGGTCAGGAAAGTACCTGGAGTACCCGGCAGGTGCCGACAGTGATCCGCA 1405

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QY 241 AGCAGCCGCGAGGAGGGCCCCAGCACCAUCCUGGAGAGCCUGUUC

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||||| 866 AGCAGCGTGAAGAGGGGCGCAAGCACCTCTTGTATCTGGAGTCTTGTTCGGAGCA 925
||| 301 GUGAUAACCAAGAGGUGGCGCGACCUUGUGGGUUCUUGUGUGAAGUACCGCGCCGC 360
||| 926 GTAATCACTAAGAAGTGGCTGATTGGTTGTTCTGTCTCTCAATATCGAGCCAGG 985
||| 361 GAGCCCGUGACCAAGGCGGAGAUUGUGGAGCGUGAUAAGAAUAUAAGACUAGCUGUUC 420
||| 986 GAGCCAGTCAAAAGGAGAAATCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTT 1045
||| 421 CCCGAGAUUCGCAAGGCGCAGCGAGAGCUCGAGCUGUGUGUUGCGCAUGGUAAG 480
||| 1046 CCTGAGATCTTCGGCAAAAGCTCTGAGTCTTGCAGCTGGTCTTGGCAATGAGTGAAG 1105
||| 481 GAGCCGACCCACCGGCCACAGCUAGUGUGUGAGACCUUGGCGGCGUGAGCUAGCAC 540
||| 1106 GAAGCAGACCCACCGGCCACTCTATGTCTTGTCTACCTGCTAGGTCTCTCTATGAT 1165
||| 541 GGCUGUGGCGGCAAAACAGAUCAUGCCCAAGACCGGCUUCUUGAUAUCUGUGUGUG 600
||| 1166 GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCTGTGATAATTGTCTGTC 1225
||| 601 AUGAUCGCCAUGGAGGCGGCCCGCCCGAGGAGGAGUUCUGGAGGAGCUGAGCUG 660
||| 1226 ATGATTGCAATGGAGGGCGGCCATGCTCTGAGGAGGAATCTGGGAGGAGCTGAGTGTG 1285
||| 661 AUGAGGUGUACAGCGCGCGAGCACAGCGCCUACCGCGAGCCCGCAAGCUGCUGAC 720
||| 1286 ATGGAGGTGTATGAGGAGGAGCAGTGCCTATGGGAGCCCGAGGAGCTGCTCACC 1345
||| 721 CAGGACCUUGUGAGGAGAAUAUCUGAGUAACCGCAGGUGCCCGACAGCACCGCC 780
||| 1346 CAAGATTTGGTCAGGAAAGTACTGAGTAGCCGAGGAGTGCAGCAGTGTATCGCGCA 1405
||| 781 CGCUACAGUUCUGUGGGGCGCCCGCGCUGGCGGAGCAGCAGCAGCAGCAGCUG 840
||| 1406 CGCTATGAGTTCTGTGGGTCCAAAGGCGCTCTGAAACCACTATGTGAAAGTCTT 1465
||| 841 GAGUACGUAUCAAAGGAGGCGCGCGGUGGCUUCUUCUCCAGCUGCGCGAGGCC 900
||| 1466 GAGTATGTATCAAGGTCAAGTGCAGAGTTCGCTTTTCTTCCATCCCTGCGTGAAGCA 1525
||| 901 GCCUCGCGGAGGAGGAGGCGGUGUGAGCCUGA 936
||| 1526 GCTTTGAGAGAGGAGGAAGAGGAGTCTGAGCATGA 1561
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RESULT 2

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US-11-178-134-6
; Sequence 6, Application US/11178134
; Publication No. US20060019290A1
; GENERAL INFORMATION:
; APPLICANT: University of Pittsburgh - of The Commonwealth System of
; APPLICANT: Higher Education
; APPLICANT: Godfrey, Tony
; APPLICANT: Hughes, Steven
; APPLICANT: Xi, Liqiang
; APPLICANT: Gooding, William E
; APPLICANT: Raja, Siva E
; TITLE OF INVENTION: Identification of Markers in Esophageal Cancer, Colon Cancer,
; FILE REFERENCE: 030160
; CURRENT APPLICATION NUMBER: US/11/178,134
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: 60/586,599
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/587,019
; PRIOR FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 1722
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; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-178-134-6
Query Match 68.2%; Score 640; DB 12; Length 1722;
Best Local Similarity 67.3%; Pred. No. 1.8e-124;
Matches 630; Conservative 121; Mismatches 185; Indels 0; Gaps 0;
Qy 1 AUGAGCCUGAGCAGCGCAGCUGACUAGCAAGCCCGAGGAGGCCUUGAGGGCCCGAGCAG 60
Db 188 ATGCTCTTTGAGCAGAGGAGTCTGCATCTGCAAGCCTGAGGAAGCCCTTGGAGCCCAAA 247
Qy 61 GAGGCCUUGGGCUGUGUGUGCAGGCGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCUG 120
Db 248 GAGGCCCTGGCCTGGTGTGTGTCAGGGTGCCTCTCTCTCTCTCTCTCTCTCTCTCTG 307
Qy 121 GGCACCCUGAGAGAGGUGCCACCGCGCGCAGCACCGACCCCGCCAGAGCCCGCCAGGGC 180
Db 308 GGCACCCUGAGAGAGGUGCCACCGCGCGCAGCACCGACCTCTCTCTCTCTCTCTCTCT 367
Qy 181 GCCAGCGCCUUCGCCACCAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUA 240
Db 368 GCCTCGCCCTTTCCTCACTACCATCACTCTGAGAGGCAACCCAGTGTGAGGTTC 427
Qy 241 AGCAGCGCGAGGAGGCGGCCCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 300
Db 428 AGCAGCGCGTGAAGAGGAGGCGGCCAAGCACCTCTGTATCTCTGTGAGTCTTGTTCG 487
Qy 301 GUGAUAACCAAGAGGUGGCGCGACCUUGUGGGGCUUCUUGCUGCUGAUAUAUAUAUAUA 360
Db 488 GTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTCTCTCTCTCTCTCTCTCTCTCT 547
Qy 361 GAGCCCGUGACCAAGGCGGAGUAGUGGAGAGCGUGAUAUAUAUAUAUAUAUAUAUAUA 420
Db 548 GAGCCAGTCAAAAGGCGAGAAATGCTGAGAGTGTATCAAAAATTACAAGCACTGTGTT 607
Qy 421 CCCGAGAUUCUGGCGAGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 480
Db 608 CCTGAGATCTTCGGCAAAAGCCTCTGAGTCTCTGAGCTGGTCTTTGGCATTTGAGTGA 667
Qy 481 GAGCGCGACCCACCGCGCCACAGCUAGCUGUGGUGAGACCUUGCUGGGGCCUUGAGCAG 540
Db 668 GAAGCAGACCCACCGCGCCACTCTATGTCTCTTGTCTACCTGCTCTCTCTCTCTCT 727
Qy 541 GGCUGUGGCGGAGCAACAGAUUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUA 600
Db 728 GGCCTGCTGGGTGATAATCAGATCATGCCCCAAGCAGGCTTCTGTGATAATTGTCTG 787
Qy 601 AUGAUCGCCAUGAGGCGCGCCACCGCGCGAGGAGAGAUUCUGGAGGAGCAGCAGCUG 660
Db 788 ATGATTGCAATGGAGGCGCGCCATGCTCTCTGAGAGGAAATCTGGGAGGAGCTGAGTGT 847
Qy 661 AUGAGGUGUAUCGACCGCGCCCGAGCAGCAGCGCCUACCGCGAGCCCGCCAGCUGCAG 720
Db 848 ATGGAGGTGTATGATGGGAGGAGCAGTGCCTATGGGAGGCCCGCAGGAGCTCTCACC 907
Qy 721 CAGGACCUUGUGCAGGAGAAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUA 780
Db 908 CAAGATTTGGTGCAGGAAAGTACTCTGGAGTACCGGCAAGTGTGCGGAGCAGTGTATCG 967
Qy 781 CGCUACAGUUCUUGUGGGGCGCCCGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 840
Db 968 CGCTATGAGTTCCTGTGGGTTCGAAGGGCCCTTGTCTGAAACCACTATGTGAAAGTCT 1027
Qy 841 GAGUACGUAUCAAAGGUGAGCGCGCGGUGGCGCUUCUUCUCCCGAGCUGCGAGGCC 900
Db 1028 GAGTATGTATCAAGGTCACTGCAAGAGTTCGCTTTTCTTCTCTCTCTCTCTCTCT 1087
Qy 901 GCCUCGCGCAGGAGGAGGCGGUGUGAGCCUGA 936
Db 1088 GCTTTGAGAGAGGAGGAAGAGGAGTCTGAGCATGA 1123
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; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 946082
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-946082

Query Match      21.3%; Score 200; DB 6; Length 604;
Best Local Similarity 58.0%; Pred. No. 6.6e-33;
Matches 268; Conservative 42; Mismatches 131; Indels 21; Gaps 1;

Qy 1 AUGAGCCUGGAGCAGCGCCUGCAUGCAAGCCCGAGAGGCCUGGAGGCCAGCAG 60
Db 143 ATGCTCTTGAGCAGAGAGTCAGCACTGCAAGCTGAGGAAGCGCTTGACACCCAAAGAA 202
Qy 61 GAGGCCUGGCGUGGUGUGCGUGCAGCGCCGCCACCG-----C 99
Db 203 GAGGCCCTGGGCCCTGGTGGGTGTGCAGGCTGCCACTACTGAGGAGCAGGAGGCTGTGTC 262
Qy 100 AGCAGCAGCCCGCCUGGUGCGGACCCUGCAGGAGGUGCCACCGCGCGCAGCAGCCGAC 159
Db 263 TCCTCTCTCTGCTGGTCCAGGACACCTCTGGGGAGGTGCTGTGCTGGTTCACCAAGT 322
Qy 160 CCCCCCAGAGCCCGCCAGGCGCCAGGCGCCUUCGCCACCAUACAUAUCCAGCCGCGAG 219
Db 323 CCTCTCAAGAGTCTCAGGAGGCGCTCCGCCATCCCACTGCCATCGATTTCACTCTATGG 382
Qy 220 CGCCAGCCAGCGAGGCGCAGCAGCGCCGAGGAGGAGGCGCCAGCAGCAGCUGCAUC 279
Db 383 AGGCAATTCATTAAAGGGCTCCAGCAACCAAGAAGAGGAGGCGGCAAGCACCTCCCTGAC 442
Qy 280 CUGGAGAGCCUGUUCGCGCGUGAUCAACCAAGAAGUGGCGCAGCCUGGUGGCGUUCUG 339
Db 443 CCAGAGTCTGTGTTCCGAGCAGCACTCAGTAAGAAGGTGGCTGACTTGATTCATTTCG 502
Qy 340 CUGUGAAGUACCGCGCCCGCAGCCCGUGAGCCAGGCCAGAGCGGAGGUGGAGGAGCUGAUC 399
Db 503 CTCCTCAAGTATTAAAGTCAAGGAGCGCGGTCAAAAGGCAGAAATGCTGGAGAGMTGTCATC 562
Qy 400 AAGAACUACAGCAGCUGUCCCGCAGAUUCCGCAAGGCC 441
Db 563 AAAAATACAGCGCTGCTTTCTCTGTGATCTTCGGCAAGGCC 604

RESULT 9
US-09-925-065A-349229
; Sequence 349229, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20

; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 946082
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-349229

Query Match      21.2%; Score 198.6; DB 6; Length 560;
Best Local Similarity 50.6%; Pred. No. 1.3e-32;
Matches 273; Conservative 62; Mismatches 195; Indels 9; Gaps 1;

Qy 158 ACCCCCCCAGAGCCCCCAGGCGCCAGCGCCUUCGCCACCAUACAUCACCCGCC 217
Db 16 ATCCTCCCCAGAGTGTCTCAGATAGCTGTCTCTCCCTCGTGTGCTTCCCTTCAT 75
Qy 218 AGCGCCAGCCCGCAGGAGGCGCAGCAGCGCCGAGGAGGAGGCGCCCGAGCAGCAGCAGCAG 277
Db 76 TAGATCAATCTGATAGGGCTCCAGCAGCCAAAGAGGAGAGTCCCAAGCACCTACAGG 135
Qy 278 UCCUG-----GAGAGCCUGUUCGCGCCCGUGAUCAACAAGAGGUGGCGCAGCUGG 328
Db 136 TCCTGCCAGACAGTGTCTTTACCCAGAAAGTGAGATAGATGAAAGAGTGACTGATTTGG 195
Qy 329 UGGGUUCCUGUGUGCAAGUACGCGCCCGCGAGCCCGUGACCAAGGCCGAGUAGCUGG 388
Db 196 TGCAGTTTCTGCTTCTCAAGTATCAATGAAGAGGCGGATCACAAAAGCGAGAATACTCG 255
Qy 389 AGAGCGUACAAGAACUACAAGCAGCUGCUUCCGAGAUUUCGCAAGGCCAGCGAGA 448
Db 256 AGAGTGTCAATAAATATTGAAGACCACTTCCCTTTGTTGTAGTGAAGCCTCCGAGT 315
Qy 449 GCCUGCAGCUGGUGUGCAUCGAGCAGGAGGAGGCGGACCCACCGGCCAGCAGCAGCAG 508
Db 316 GCATGCTGCTGCTTTGGCATTTGATTAAGGAAGTGGATCCCACTTGGCCACTCTCTTTG 375
Qy 509 UGCUUGAGCUGCCUGGCGCUGAGCUACGACGCGCUGGUGGCGCAACCAAGCAUAGC 568
Db 376 TCCTTGTGACCTCCCTGGGCTTCCCTATGATGGATGCTGAGTGTCCAGAGCATGC 435
Qy 569 CCAAGACCGCUUCCUGAUCAUCGUGUGUGUGAUUGCGCAUGGAGGCGGCGCACGCC 628
Db 436 CCAAGACTGGCATTTCTCATACTTATCTTAAGCATAGTCTTTCATAGAGGGCTACTGCACCC 495
Qy 629 CCGAGGAGGAGUUCUGGAGGAGGAGCUGAGCUGGAGGUGGUGUACGACGGCGCGAGCAG 687
Db 496 CTGAGGAGGTCACTGGGAAGCACTGAATATATGATGGGCTGTATGATGGATGGAGCAG 554

RESULT 10
US-09-925-065A-349230
; Sequence 349230, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 946082
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-946082
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; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 349230
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-349230

Query Match 21.2%; Score 198.6; DB 6; Length 560;
Best Local Similarity 50.6%; Pred. No. 1.3e-32;
Matches 273; Conservative 62; Mismatches 195; Indels 9; Gaps 1;

QY 158 ACCCCCCCAGAGCCCCAGGGCGCCAGCGCCGCGAGGAGGAGGCCCCAGCACCAUACUACCCGCC 217
Db 16 ATCTCTCCAGAGTGCTCAGATAGCT 75

QY 218 AGCGCCAGCCCCAGGAGGCGAGCAGCAGCGCGAGGAGGAGGCCCCAGCACCAUACUACGCA 277
Db 76 TAGATCAATCTGATGAGGGCTCCAGCAGCCAAAGAGGAGGAGTCCAAAGCACCTTACAGG 135

QY 278 UCCUG-----GAGAGCCUUGUCCGCGCGGUGAUCACCAAGAGUGGCGCGACCUGG 328
Db 136 TCCTGCCAGACAGTGAGTCTTTTACCAGAAAGTGAGATGATGATGATGATGATGATGATGAT 195

QY 329 UGGGCUUCUGUGUGAGUACCGCGCGCGAGCCGCGAGCCGUGACCAAGGCGGAGUUGCG 388
Db 196 TGCAGTTTCTGCTCTTCAAGTATCAAAATGAAGGAGCGGATCACAAAGGAGAGAAATACTGG 255

QY 389 AGAGCGUAGUACAAAGACUACAGACUACUCCCGAGUACUUCGCGCAAGGCGAGCGAGA 448
Db 256 AGAGTGCTAAGAAATATGAGACCACTTCCCTTTGTTGTTAGTGAAGCTCCGAGT 315

QY 449 GCUUGCAGUGUGUUCGCGUACGUGAGGAGGCGCGAGCCCGACCCCGCGCACGACUACG 508
Db 316 GCATGCTGCTGCTTTGGCATTTGATGTAAGGAAGTGGATGATGATGATGATGATGATGATGAT 375

QY 509 UCUUGUACUGGCGGCGUGAGUACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 568
Db 376 TCCTTGTCACTTCCCTGGGCGTCACTATGATGATGATGATGATGATGATGATGATGATGATGAT 435

QY 569 CCAAGACGGGCUUCUGUACUACUGUGUGUAGUACGCGCAUGGAGGCGGCGGCGGCGGCGG 628
Db 436 CCAAGACTGGCATTTCTACTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTAT 495

QY 629 CCGAGGAGAGUACUGGAGGAGGAGUACGUGAGGUGUAGUACGAGCGGCGGCGGCGGCGG 687
Db 496 CTGAGGAGTCACTGGGAAGCACTGAATATGATGGGCTGTATGATGGGATGGAGCAC 554

RESULT 11
US-11-044-051-72
; Sequence 72, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, Danisle
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR FILING DATE: US 60/459,263
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 1983
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1329)..(1329)
; OTHER INFORMATION: n at position 1329 is "a" in MAGE-C2 and "g" in CT10
US-11-044-051-72

Query Match 21.1%; Score 198.4; DB 12; Length 1983;
Best Local Similarity 49.3%; Pred. No. 1.3e-32;
Matches 307; Conservative 72; Mismatches 232; Indels 12; Gaps 3;

QY 311 AGAAGUGGCGGACCGUGUGGCGCUUCUGUGUAGUACCGCGCGCGCGAGCCGUGA 370
Db 757 AAAAGGTGGCGGAGTTAGTGAGTCT 816

QY 371 CCAAGGCGGAGUACUACAGGAGGAGUACAGAACUACAGCACUUGUCCCGGAGUACU 430
Db 817 CAGAGGCGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 873

QY 431 UCGGCAAGGCGAGGAGGCGUGCAGUGUGUGUUCGCGCAUCGAGGAGGAGGCGGAGCC 490
Db 874 TCAAGAGGCGCGTGAGTTCATGAGGCTCTTTTGGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 933

QY 491 CCACCGGCGCAGUACUGUGUGUGAGCCUGGCGUGGCGUGAGUACGACGCGCGUGCG 550
Db 934 ---CTGACCACTTCTGTGTGTTTGCAGAACACAGTAGGCTTCCAGGATGAGGG---TA 984

QY 551 GCGACACACAGUACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 610
Db 985 GTGATGATGAGGCGCATGCGCGAGAACAGGCTCTCTGATTTATTTCTGAGTGTGATCTTTCA 1044

QY 611 UGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 670
Db 1045 TAAAGGCGCACTGTGCTCTGTGAGGAGTCTCTGGAAGTCTGGAAGTCTGGAAGTCTGGAAGT 1104

QY 671 ACAGCGCGCGGAGCAGCAGCGCCUACGCGGAGCCCGCGAGCGGCGGCGGCGGCGGCGG 730
Db 1105 ATGCTGGGAGGAGCACTTCTGTCTATGGGAGGCGCTAGGAGGCTCTCTCACTAAAGTTTGGG 1164

QY 731 UGAGGAGAGUACUACGCGGAGUACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 790
Db 1165 TGCAGGAGCACTTACCTGGAGTATCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1224

QY 791 UCUUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 850
Db 1225 TCTGTGGGTCCAGAGGCCCATTCAGAAAGCATCAGAAAGCATCAGAAAGCATCAGAAAGCAT 1284

QY 851 UCAAGGUGAGCGCGCGGUGGCGCUUCUUCUCCAGCGCGGCGGCGGCGGCGGCGGCGG 910
Db 1285 CCAAGCTGAACAACACTGTTCTAGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1344

QY 911 AGGAGGAGGCGGCGGUGAGGCC 933
Db 1345 ATGTGAAGAGAGAGTCCAGGCC 1367

RESULT 12
US-11-044-051-104
; Sequence 104, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, Danisle
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR FILING DATE: US 60/459,263
; NUMBER OF SEQ ID NOS: 111

Db 735 GCAGGCTTACCAGAAACGGATGGGAGTGCATAATGCAGCGATTCAAGTGATC 785

RESULT 3
US-09-762-861B-1
; Sequence 1, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
; CURRENT APPLICATION NUMBER: US/09762,861B
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, x = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
; US-09-762-861B-1

Query Match 62.9%; Score 487.4; DB 3; Length 1023;
Best Local Similarity 76.9%; Pred. No. 1.8e-83;
Matches 593; Conservative 1; Mismatches 177; Indels 0; Gaps 0;

Qy 1 AGATCTAAAGATGACCTGTGACCGAGGTGGAGACCTTACTGTGTGAGCATCATCCCCAG 60
Db 15 ATATTTAAAGATGAGTCTTCTGACCGAGGTGCAACGTTACGTTCTCTCTATCGTACCATC 74
Qy 61 CGGCCCCCTGAAGCCGAGATCGCCAGAGGCTGGAGACGTGTTGCGCCGCAAGAAC 120
Db 75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGCTTTTGCAGGGGAAGAAC 134
Qy 121 CGACTGAGGTGCTGTGATGGAGTGGCTGAAGACAGGCCCCATCTGAGCCCCCTGACCAA 180
Db 135 CGATCTTGAGGCACTCATGGAATGGCTTAAGACAGACCAATCTGTCACTCTGACTAA 194
Qy 181 GGGCATCTGGGCTTCGTGTTCACTGACCGTCCAGCGAGCGCGCTTCGACGCGCG 240
Db 195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTCCAGTGGAGGAGTTCGAGCGGTAG 254
Qy 241 CGCTTGTGAGAACGCCCTGAACGGCAACGGCGACCCCAACCAACATGGAACAGGCGGT 300
Db 255 ACGCTTTGTCAAAATGCCCTTAGTGGAAACGGAGATCCAAACCAACATGGACAGAGCAGT 314
Qy 301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACTTCCAGCGGCCCAAGGAGATCAGCCT 360
Db 315 AAAAGTGTACAGGAAGCTTAAAGAGAAATTAACATTCATGGGGGAAAAGGTTGGACT 374
Qy 361 GAGCTACAGCGCGCGCTTCGGCAGCTGATGGGCTGATCTACAAACAGGATGGGCGC 420
Db 375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCTGGAAGTCTATATACACAGAAATGGGAAC 434
Qy 421 CGTGACACCGAGGTGGCTTCGGCGCTGGTGTGGCCACCTTCGAGACGATCGCGCAGAC 480
Db 435 TGTGACAAACCGAAGTGGCAATTTGGCGCTTGSTATGCGCCACATGTGAAACAGATCGTGTTC 494

Qy 481 CCAGCACCGCAGCCACAGGAGATGGTGACCAACCAACCCCTGTATCAGGCGACGAGAA 540
Db 495 CCAGCATCGATCTCACAGGCGAGATGGTGACAAACAACCAACCCATTAATCAGACATGAAA 554
Qy 541 CAGGATCGTGTGCGCAGACCAACCGCAAGGCCATGAGCAGATGSCCGCAGCAGCGA 600
Db 555 CAGAATCGTATTAGCCAGTACCAGCGCTAAAGCCATGGAGCAGATGGCAGGGTCAGTGA 614
Qy 601 GCAGGCCCGCAGGAGCCATGAGGTGGCGCAGCAGGCGAGGAGATGGTGACAGGCGCATGAG 660
Db 615 GCAGGCGAGCAGGCGCATGGAGTTGCTAGTAAGGCTAGGCGAGATGGTRCAGGCAATGAG 674
Qy 661 GACCATCGGCAACCCACCCAGCAGCAGCGCGGCTGAAGAACCACTGTGTGAGAACCT 720
Db 675 AACCATTTGGGACCCACCCCTAGCTCCAGTCCGCGTTTGAAGATGATCTCTCTTGAATAAT 734
Qy 721 GCAGGCTTACCAAGAGCGCATGGCGTGCAGATGCGAGGCTTCAAGTGAAC 771
Db 735 GCAGGCTTACCAAGAGCGATGGGAGTGCATAATGCAGCGATTCAAGTGATC 785

RESULT 4
US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, x = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
; US-10-065-133A-1

Query Match 62.9%; Score 487.4; DB 3; Length 1023;
Best Local Similarity 76.9%; Pred. No. 1.8e-83;
Matches 593; Conservative 1; Mismatches 177; Indels 0; Gaps 0;

Qy 1 AGATCTAAAGATGACCTGTGACCGAGGTGGAGACCTTACTGTGTGAGCATCATCCCCAG 60
Db 15 ATATTTAAAGATGAGTCTTCTGACCGAGGTGCAACGTTACGTTCTCTCTATCGTACCATC 74
Qy 61 CGGCCCCCTGAAGCCGAGATCGCCAGAGGCTGGAGACGTGTTGCGCCGCAAGAACAC 120
Db 75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGCTTTTGCAGGGGAAGAAC 134
Qy 121 CGACTGAGGTGCTGTGATGGAGTGGCTGAAGACAGGCCCCATCTGAGCCCCCTGACCAA 180
Db 135 CGATCTTGAGGCACTCATGGAATGGCTTAAGACAGACCAATCTGTCACTCTGACTAA 194
Qy 181 GGGCATCTGGGCTTCGTGTTCACTGACCGTCCAGCGAGCGCGCTTCGACGCGCG 240
Db 195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTCCAGTGGAGGAGTTCGAGCGGTAG 254

Qy 241 CCGCTTCGTGCAGAACCCCTGAACGCAAGCGGACCCCAACCAACATGACAAAGCCGT 300
Db 255 ACGCTTTGTCCAAATGCCCTTAGTGGAACCGGAGATCCAAACCAACATGACAGAGCAGT 314
Qy 301 GAAGCTGTACAGGAAGCTGAAGAGGAGATCACCTTCCACGGCGCCAAAGGAGATCAGCCT 360
Db 315 AAAAAGCTGACAGGAAGCTTAAAGAGAAATAACATTCATCGGGCAAAAGGTTGGCACT 374
Qy 361 GAGCTACAGCGCGCGCCCTGGCCAGCTGCATGGGCTGATCTACAAACAGGATGGCGC 420
Db 375 CAGCTATTCACCTGGTGCACCTAGCCAGCTGCATGGGACTCATATACAAACAGATGGGAAC 434
Qy 421 CGTGACACCGAGGTGGCCCTTGGCCCTGGTGTGGCCACCTGCAGAGCAGATCGCCGACAG 480
Db 435 TGTGACAAACGGAAGTGGCAATTTGGCCCTGGTATGGCCACATGTGAAACAGATCGCTGATTC 494
Qy 481 CCAGCAGCGGACGACAGGAGATGGTGACCAACCAACCAACCCCTGATCAGGACAGGAA 540
Db 495 CCAGCATCGATCTCACAGGAGATGGTGACAAACCAACCAACCCATTAATCAGACATGAAA 554
Qy 541 CAGGATGGTGTGGCCAGCACCCAGCCAGGCGCATGGAGCAGATGGCCGCGCAGCAGCGA 600
Db 555 CAGAATGGTATTAGCCAGTACCAACCGCTTAAAGCCATGGAGCAGATGGCGGTGAGTGA 614
Qy 601 GCAGGCCGCGAGGCCATGAGGTGGCCAGCAGCAGCCAGCAGCAGATGGTGAGGCCATGAG 660
Db 615 GCAGGCAGCAGAGGCCATGAGGTGGTGTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAG 674
Qy 661 GACCATCGGACCCACCCAGCAGCAGCGCGGCTGAAGAAACGACCTGCTGGAGAACCT 720
Db 675 AACCATGGGAGACCCACCCCTAGCTCCAGTGCCGGTTGAAAGATGATCTCCTTGAATAAT 734

RESULT 5

US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (663)..(663)
; OTHER INFORMATION: At nucleotide 663, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-434-811A-1

Query Match 62.9%; Score 487.4; DB 3; Length 1023;
Best Local Similarity 76.9%; Pred. No. 1.8e-83;

Matches 593; Conservative 1; Mismatches 177; Indels 0; Gaps 0;
Qy 1 AGATCTAAAGATGAGCCTCTGACCGAGGTGGAGACTAGTGTGCTGAGCATCATCCCCAG 60
Db 15 ATATTTAAAGATGAGTCTTCTGACCGAGGTGGAACGTACGTTCTCTCTATCGTACATC 74
Qy 61 CGSGCCCTTGAAAGGCGAGATCGCCAGAGGCTGGAGGACGTGTTCCGCGGCAAGAACAC 120
Db 75 AGSCCCCTTCAAGCCGAGATCGCGCAGAGACTTGAAGATGCTTTTGACGGGAGAACAC 134
Qy 121 CGACCTTGGAGGTGCTGATGGAGTGGCTGAAGACAGGCCCCATCTGAGGCCCCCTGACCAA 180
Db 135 CGATCTTGGAGCACTCATGGAATGGCTTAAAGACAAGACCAATCTCTGCACTCTGACTAA 194
Qy 181 GGGCATCTCGGGCTTCTGTTTCACTGACCTGACCTGCGCCAGGAGCGGCGCTGACGCGCG 240
Db 195 AGGGATTTTAGGATTCGTATTTCACGCTCACCGTGCCTGAGCGAGGACTGCGAGCGTAG 254
Qy 241 CCGCTTCGTGCAGAACCGCCTGAACCGCAACGGCGACCCCAACCAACATGACAAAGCCGT 300
Db 255 ACGCTTTGTCCAAATGCCCTTAGTGTAAACGGAGATCCAAACCAACATGACAGAGCAGT 314
Qy 301 GAAGCTGTACAGGAAGCTGAAGAGGAGATCACCTTCCAGCGGCGCAAGAGAGATCAGCCT 360
Db 315 AAACTGTACAGGAAGCTTAAAGAGAGAAATAACATTCATGGGGCAAAAGAGGTGGCACT 374
Qy 361 GAGCTACAGCGCGCGCGCCTTGGCCAGCTGCATGGGCTGATCTACAAACAGGATGGCGC 420
Db 375 CAGCTATTCCACTGGTGCACCTAGCCAGCTGCATGGGACTCATATACAAACAGATGGGAAC 434
Qy 421 CGTGACCAACCGAAGTGGCATTTGGCTGTGATGCGCCACATGTGAACAGATCCCTGATTC 494
Db 481 CCAGCAGCGCAGCCACAGCAGATGGTGACCAACCAACCCCTGATCAGGCAACGAGAA 540
Db 495 CCAGCATCGATCTCACAGGCAGATGGTGACAAACCAACCCATTAATCAGACATGAAAA 554
Qy 541 CAGGATGGTGTGGCCAGCAACCCGCAAGGCCATGGAGCAGATGGCCGCGCAGCAGCGA 600
Db 555 CAGAATGGTATTAGCCAGTACCAACCGCTTAAAGCCATGGAGCAGATGGCGGGTGCAGTGA 614
Qy 601 GCAGGCCGCGGCGCCATGAGGTGGCCAGCAGGCGCAGGCGCAGATGGTGAGGCGCATGAG 660
Db 615 GCAGGCAGCAGAGGCCATGAGAGTTGCTAGTAGGCTAGGCAGATGGTRCAGGCAATGAG 674
Qy 661 GACCATCGGACCCACCCAGCAGCAGCGCGCTGAAAGAACGACCTGCTGGAGAACCT 720
Db 675 AACCATTTGGGACCCACCCCTAGCTCCAGTGCCGGTTTGAAGATGATCTCCTTGAATAAT 734

RESULT 6

US-08-809-513A-6
; Sequence 6, Application US/08809513A
; Patent No. 6524588
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
; TITLE OF INVENTION: Method
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NORRIS McLAUGHLIN & MARCUS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:

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/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
/ COMPUTER: Gateway Pentium II
/ OPERATING SYSTEM: Windows 98
/ SOFTWARE: Word 97
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/909,513A
/ FILING DATE: 24-MAR-1997
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/EP95/03663
/ FILING DATE: 18-SEP-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 94115505.3
/ FILING DATE: 30-SEP-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kurt G. Briscoe
/ REGISTRATION NUMBER: 33,141
/ REFERENCE/DOCKET NUMBER: Hobom 9832-KGB
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (914) 332-1700
/ TELEFAX: (914) 332-1844
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6802 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: circular
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Influenza virus, RNA sequence
/ INDIVIDUAL ISOLATE: pHL1191
/ US-08-809-513A-6

Query Match 62.8%; Score 486.6; DB 3; Length 6802;
Best Local Similarity 77.3%; Pred. No. 3.1e-83;
Matches 591; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

Qy 7 AAAGATGAGCTGTGACCGAGGTGGAGACCTAGTGTGAGCATATCCCGAGGGCC 66
Db 34 AAAGATGAGTCTTAAACCGAGGTGCGAAACGTACGTTCTCTATCATCCCGTCA 93
Qy 67 CCTGAAGCCGAGATCGCCAGAGGCTGGAGAGCTGTTCGCCGCGAAGAACACCGACCT 126
Db 94 CCTCAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTCAGGAGAGAACCGATCT 153
Qy 127 GGAGGTGCTGATGGAGTGGCTGAAGACACGAGCCCATCTGAGCCCCCTGACCAAGGGCAT 186
Db 154 TGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACTCTGACTAAGGGAT 213
Qy 187 CTGGGCTTGCTGTTTCAACCTGACCGTCCAGCGAGCGCGGCTGAGCGCCGCGTT 246
Db 214 TTTAGGATTTGTGTTTCAAGCTCAAGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 273
Qy 247 CGTCAGAACGCTGAGCGGCAAGCGGACCCCAACCAATGACCAAGCGCGTGAAGCT 306
Db 274 TGTCCAAATGCCCTTAAATGGGACGGGATCCAAATGAATGAACAGCAGTTAAACT 333
Qy 307 GTACAGGAAGCTGAAGAGGAGATCACCTTCCAGCGGCCCAAGGAGATCAGCCTGAGCTA 366
Db 334 GTATAGGAAGCTCAAGAGGAGATAACATTCATGGGGCCAAAGAAATCTCACTCAGTTA 393
Qy 367 CAGCGCGGCGCTTGGCCAGCTGATGAGGCTGATCTAACAAGGATGGCGCGCGTGAC 426
Db 394 TTCTGCTGGTGCATTTGCGAGTTGTATGGGCTCATATACACAGGATGGGGGTGTGAC 453
Qy 427 CACCGAGTGCCTTCGCGCTGTGTGCGCCACCTCGCAGCAGATCGCCGACACGACGA 486
Db 454 CACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAAACAGATTCCTGACTCCACGA 513
Qy 487 CCGAGGCCACAGGAGATGGTGACCAACCAACCCCTGATCAGGCGACAGGAACAGGAT 546
Db 546 CCGAGGCCACAGGAGATGGTGACCAACCAACCCCTGATCAGGCGACAGGAACAGGAT 546

RESULT 7
US-09-506-286B-4
; Sequence 4, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
US-09-506-286B-4

Query Match 62.5%; Score 484.6; DB 3; Length 1023;
Best Local Similarity 76.8%; Pred. No. 5.9e-83;
Matches 592; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

Qy 1 AGATCTTAAGATGAGCTGTGACCGAGGTGGAGACCTAGCTGCTGAGCATATCCCCAG 60
Db 15 ATATTTAAAGATGAGTCTTCTGACCGAGGTGCGAAACGTAGCTTCTCTATCTTACCATC 74
Qy 61 CGGCCCCCTCAAGGCCGAGATCGCCACAGAGGCTGGAGAGCTGTTCCGCGCAAGAACAC 120
Db 75 AGGCCCCCTCAAGGCCGAGATCGCGCAGAGACTTGAAGATGCTTTTCAGGAGAACAC 134
Qy 121 CGACTCGAGGTGCTGATGAGTGGCTGAAGACCAGGCCCATCTCTAGCCCCCTTGACCAA 180
Db 135 CGATCTTGAGGCACTCATGGAATGGCTTAAAGACAAGACCAATCCTGTCACTCTGACTAA 194
Qy 181 GGGCATCTGGGCTTGGTGTTCACCTGACCGTCCCGAGGAGCGCGCTGACGCGCG 240
Db 195 AGGATTTTAGGATTCGTATTCACGCTCACCGTCCCGAGGAGGAGGAGGAGGAGGAG 254
Qy 241 CCGCTTCGTGAGAACCGCCCTTGAACCGGCAACCGCGACCCCAACCAATGGAACAAGGCGGT 300
Db 255 ACGCTTTGTCNAAATGCCCTTAGTGAACCGGAGATCCAAACCAACATGACAGAGCAGT 314
Qy 301 GAAGCTGTACGGAAGCTGAAGAGGAGATCACTTCCAGCGGCCCAAGGAGATCAGCCT 360
Db 315 AAAACTGTACAGGAAGCTTAAAGAGAAATAACATTCATCCATGGGGCAAAAGAGGTGGCACT 374
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Qy 361 GAGCTACAGCGCGCGCCCTGGCCAGCTGATGGGCTGTATCTAACAGGATGGCGC 420
| | | | |
Db 375 CAGCTATTCCACTGGTGCACCTAGCCAGCTGATGGGACTCATATACACAGAATGGGAAC 434
| | | | |
Qy 421 CGTGACACCGAGGTGGCCCTCGGCCCTGGTGTGCGCCACCTGGCGAGCAGATCGCGCAG 480
| | | | |
Db 435 TGTGACAAACGAAAGTGGCAATTGGCCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494
| | | | |
Qy 481 CCAGCAGCGGAGCCACAGGAGATGGTGCACCAACCAACCCCTGTATAGGCGACGAGAA 540
| | | | |
Db 495 CCAGCATCGATCTCACAGCAGATGGTGCACATTAACCAACCCATTAATCAGACATGAAGA 554
| | | | |
Qy 541 CAGATGGTGTGCGCCAGCAGCACCGCCAGGCGCATGGAGCAGATGGCGCGGAGCAGCGA 600
| | | | |
Db 555 CAGAAATGGTATTAGCCAGTACACCGGCTAAAGCCATGGAGCAGATGGCGGGTGCAGTGA 614
| | | | |
Qy 601 GCAGGCGCGAGGCCATGGAGGTGGCCAGCCAGGCGCAGATGGTGCAGGCGCATGAG 660
| | | | |
Db 615 GCAGGCGAGCAGAGGCCATGGAGGTGGTGTAGTGAAGGCTAGGCGAGATGGTACAGGCAATGAG 674
| | | | |
Qy 661 GACCATCGGCAACCAACCCAGCAGCGCGCGCTGAAGAACGACCTGTGTGAGAAACCT 720
| | | | |
Db 675 AACATTGGGACCCACCTAGCTCCAGTGCAGGTTTGAAGATGATCTCCTTGAATTT 734
| | | | |
Qy 721 GCAGGCTACAGAAAGCGCATGGCGGTGCGAGATGACGGCTTCAAGTGAAC 771
| | | | |
Db 735 GCAGGCTACAGAAACGGATGGGAGTGCAAAATGCAGCGATTCAAGTGATC 785
| | | | |

RESULT 8

US-09-762-861B-4
; Sequence 4, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS (formerly HK2-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
US-09-762-861B-4

Query Match 62.5%; Score 484.6; DB 3; Length 1023;
Best Local Similarity 76.8%; Pred. No. 5.9e-83;
Matches 592; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

Qy 1 AGATCTAAAGATGAGCGCTGTGACCGAGGTGGAGACCTACGCTGTGAGCATCATCCCCCAG 60
| | | | |
Db 15 ATATTTAAAGATGAGTCTTCTGACCGAGGTGGAACGTACGTTCTCTATCTTACCATC 74
| | | | |
Qy 61 CGGCCCCCTGAAGCCGAGATGCGCCAGAGGCTGAGGACGTGTTGCGCGGCAAGAAC 120
| | | | |
Db 75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGCTTTTGCAGGGAAGAAC 134
| | | | |
Qy 121 CGACTGAGGTGTGATGGAGTGGCTGAAGACCAAGGCCCATCTCGAGCCCCCTGACCA 180
| | | | |

Db 135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACTCTGACTAA 194
| | | | |
Qy 181 GGGCATCTCTGGGCTTTCGTGTTTCACTGACCGTGCAGGAGCGGCGCTGAGCGCCG 240
| | | | |
Db 195 AGGGATTTTAGGATTCGTATTCACTGCTCACCGTGCCTCAGTGTGAGCGAGGACTGCGAGCTAG 254
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Qy 241 CCCTTTCTGTGCAAGACGCGCTGAAACGSCAACGCGCACCCCAACAAATGATGACAAGGCCGT 300
| | | | |
Db 255 ACCCTTTGTCCAAATGCGCTTGTGTAACGAGATCCAAACAACATGACAGAGAGCT 314
| | | | |
Qy 301 GAAGCTGTACAGGAAGCTGAAGAGGAGATCACTTCCACGCGGCCCAAGAGATCAGCCT 360
| | | | |
Db 315 AAACTGTACAGGAAGCTTAAAGAGAAATAAATCCATCCATGGGCAAAAAGAGTGGCACT 374
| | | | |
Qy 361 GAGCTACAGGCGCGCGCCCTGGCCAGCTGCTGATGGGCTGTATCTAACAGGATGGCGGC 420
| | | | |
Db 375 CAGCTATTCTCACTGGTGCACCTAGCCAGCTGCTGAGGACTCATATACAAAGAAATGGGAAC 434
| | | | |
Qy 421 CGTGACCAACGAGGTGGCCCTTCGCGCTGGTGTGCGCCACCTGCGAGCAGATCGCGCAG 480
| | | | |
Db 435 TGTGACAACCGAAGTGGCATTTGGCCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494
| | | | |
Qy 481 CCAGCAGCGCAGCCACAGGAGATGGTGCACCAACCAACCCCTGTATCAGGCGACGAA 540
| | | | |
Db 495 CCAGCATCGATCTCACAGGAGATGGTGCACATAACCAACCCATTAATCAGACATGAAGA 554
| | | | |
Qy 541 CAGATGGTGTCTGGCGAGCACCAACCGCCAAAGGCGATGGAGCAGATGGCGCGGAGCAGCGA 600
| | | | |
Db 555 CAGAAATGGTATTAGCCAGTACCAACCGCTAAAGCCATGGAGCAGATGGCGGGTGCAGTGA 614
| | | | |
Qy 601 GCAGGCGCGAGGCCATGGAGGTGGCCAGCGCGGCGCTGAAGAACGACCTGTGCGAGCCATGAG 660
| | | | |
Db 615 GCAGGCGAGCAGAGGCCATGGAGGTGGTGTAGTGAAGGCTAGGCGAGATGGTACAGGCAATGAG 674
| | | | |
Qy 661 GACCATCGGCAACCAACCCAGCAGCGCGCGCTGAAGAACGACCTGTGAGGAAACCT 720
| | | | |
Db 675 AACATTGGGACCCACCTAGCTCCAGTGCAGGTTTGAAGATGATCTCCTTGAATTT 734
| | | | |
Qy 721 GCAGGCTACAGAAAGCGCATGGCGGTGCGAGATGACGGCTTCAAGTGAAC 771
| | | | |
Db 735 GCAGGCTACAGAAACGGATGGGAGTGCAAAATGCAGCGATTCAAGTGATC 785
| | | | |

RESULT 9

US-10-065-133A-4
; Sequence 4, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
US-10-065-133A-4

Query Match 62.5%; Score 484.6; DB 3; Length 1023;
Best Local Similarity 76.8%; Pred. No. 5.9e-83;
Matches 592; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

Qy	1	AGATCTAAAGATGAGCCTGCTGTA	CGGAGGTGGAGACCTTACGTGCTGAGCATCATATCCCCAG	60
Db	15	ATATTTAAAGATGAGTCTTCTGAC	CGGAGGTGGAACCGTACGTTCTCTCTATCTTACCATC	74
Qy	61	CGGCCCCCTGAAGGCGGAGATCG	CCAGAGCTCGGAGGAGCTGTTCCGCCGGAAGACAC	120
Db	75	AGGCCCCCTCAAGCCGAGATCGCG	CAGAGACTTGAAGATGTCTTTGCAGGGAAGAACAAC	134
Qy	121	CGACCTGGAGGTGCTGATGGAGTG	CGCTCAAGACACAGGCCCATCTCTGAGCCCCCTGACCAA	180
Db	135	CGATCTTGAGGCACCTCTGTAATG	GGCTTAAGACAGAACCAATCTCTGTCACTCTGACTTAA	194
Qy	181	GGGCATCTCTGGCTTCGTGTTTCA	CCCTGACCGTGTCCAGCGAGCGCGGCTCTGAGGCGCG	240
Db	195	AGGGATTTTATGATTCGTATTACG	CTCACGCTCACCGTGCCAGTGCAGCGAGACTGCGAGCGTAG	254
Qy	241	CGCTTCGTGCGAAGACGCCCTGAA	CGGCAACGGCGACCCCAACAAATGACAAAGGCCGT	300
Db	255	ACGCTTTGTGCCAAATGCCCCTTA	GTGGAAACGGAGATCCAAACAAATGCACAGAGCACT	314
Qy	301	GAAGCTGTACAGGAAGCTGAAGAG	GGAGATCACCTTTCCACGGCGCCAAAGGAGATCAGCCT	360
Db	315	AAAACTGTACAGGNAAGCTTAAAG	AGAAATTAACATTCATGCGGCGCAAAAGAGGTGGCACT	374
Qy	361	GAGCTACAGCGCGCGCCTTGCCAG	CTGCATGGGCTGATCTTACAAACAGGATGGCGCG	420
Db	375	CAGCTATTCATCTGTTGCACTAGC	CAGCTGCATGGGACTCATATACAAAGATGGGAAC	434
Qy	421	CGTGACACCGAGGTGGCCTTCGG	CCTTGGCTGTGGCCACCTGCGAGCAGATCGCCGACAG	480
Db	435	TGTGACAAACGAAGTGGCATTTG	GCCCTTGGTATGCCACATGTGAACAGATCGCTGATTC	494
Qy	481	CAGACACCGCAGCACAAGGAGATG	GTGACCAACCAACCCCTTGATCAGGCACGAGAA	540
Db	495	CCAGCATCGATCTCAAGGCGAGTGG	TGACAAATAACCAACCCATTATCAGACATGAAAA	554
Qy	541	CAGGATGGTCTGGCCAGCACCAAC	CGGCCATGGAGCAGATGGCCGCGGACAGCGA	600
Db	555	CAGAAATGGTATTAGCCAGGTACA	CGGCTTAAGCCATGGAGCAGATGGCAGGGTTCGAGTGA	614
Qy	601	CGAGGCGCGCAGGCCCATGGAGTGG	CGCAGCCAGGCAGAGTGTGTGACGCCCATGAG	660
Db	615	GCAGGCAGCAGAGGCCATGGAGGTT	GTCTAGTAAAGGCTTAGGCATGGTACAGGCCAATGAG	674
Qy	661	GACCATTCGCACCCACCCACGAGC	AGCGCGCGGCTTGAAGAACCGACCTGCTGGAGAACCT	720
Db	675	AACCATTTGGGACCCACCCCTAGCT	CCAGTGCCTGGTTTGAAGATGATCTCTCTTGAAATTT	734
Qy	721	GCAGGCTTACAGAAAGCGCATGGG	CGGTGCGAGATGCAGCGCTTCAAGTGAAAC	771
Db	735	GCAGGCTTACAGAAACGGATGGAGT	GTGCAATGCAATGCAAGTTCAGTGATC	785

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: SEQ ID NO 4
:
: LENGTH: 1023
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: TYPE: DNA
:
: ORGANISM: Equine influenza virus H3N8
:
: FEATURE:
:
: NAME/KEY: CDS
:
: LOCATION: (25)..(780)
:
: OTHER INFORMATION:
:
: US-10-434-811A-4

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RESULT 11
US-09-311-784A-13
; Sequence 13, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.

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; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Cheenut, Robert W.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
; OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of
; OTHER INFORMATION: influenza matrix protein gene
; NAME/KEY: CDS
; LOCATION: (16)...(816)
; OTHER INFORMATION: PADRE-Influenza matrix
; US-09-311-784A-13

Query Match      61.6%; Score 477.4; DB 3; Length 816;
Best Local Similarity 76.8%; Pred. No. 1.3e-81;
Matches 583; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

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Qy 131 GTGCTGATGGAAGTGCCTGAAGACAGGCGCCCTCTGAGCCCTTGAACAGGGCATCTG 190
Db 178 GCTCTCATGGAATGCTTAAGACAGACCAATCTCTGTCACCTGATGAAGGAATTTTA 237

Qy 191 GGCTTGTGTTTCACTTCACTGAGCGCGCGCTGAGCGCGCGCTGAGCGCGCGCTTGTG 250
Db 238 GGGTTGTGTTTCACTTCACTGAGCGCGCGCTGAGCGCGCGCTGAGCGCGCGCTTGTG 297

Qy 251 CAGAACGCTGAAGAGGAGATCACCTTCCACGCGCGCAAGGAGATCAGGCTGAGCTACAG 310
Db 298 CAAAATGCCCTAAATGGGAATGGAGACCCCAACCAACATGAGCAGGGCAGTTAAACTATAC 357

Qy 311 AGGAAGCTGAAGAGGAGATCACCTTCCACGCGCGCAAGGAGATCAGGCTGAGCTACAG 370
Db 358 AAGAGCTGAAGAGGGAATGACATCTCCATGAGCAAGGAGATGTCATCAGTTACTCA 417

Qy 371 GCCGCGCGCTTGGCAGCTGATGGGCTGTATCTAACAGAGATGGGCGCGCTGAGCACC 430
Db 418 ACTGTTGGCTTGGCAGTTGATGGTCTCTATATACACCGGATGGGAACAGTGAACACA 477

Qy 431 GAGTTGGCTTGGCAGCTGATGGGCTGATGGGCTGATGGGCTGATGGGCTGATGGGCTG 490
Db 478 GAAATGGCTTGGCAGTTGATGGGCTGATGGGCTGATGGGCTGATGGGCTGATGGGCTG 537

Qy 491 AGCCACAGGAGATGGTGCACCAACCAACCCCTGATCAGGACAGCAAGGATGGT 550
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Qy 611 GAGGCCATGGAGGTGGCGAGCCAGGCGAGGAGATGGTGTGAGGCCATGAGGACCATCGC 670

; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Cheenut, Robert W.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
; OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of
; OTHER INFORMATION: influenza matrix protein gene
; NAME/KEY: CDS
; LOCATION: (16)...(816)
; OTHER INFORMATION: PADRE-Influenza matrix
; US-09-311-784A-13

Query Match      61.6%; Score 477.2; DB 3; Length 756;
Best Local Similarity 76.9%; Pred. No. 1.4e-81;
Matches 581; Conservative 1; Mismatches 174; Indels 0; Gaps 0;

Qy 11 ATGAGCTGTGACCGAGGTGGAGACCTACGTGTGTGAGCATCATCCCGAGCGGCCCTG 70
Db 1 ATGAGTCTTCTGACCGAGGTGGAACGTACGTCTCTATCTATCTGATCAGGCCCTC 60

Qy 71 AAGCGGAGATCGCGCAGAGCTGGAGAGCGTGTTCGCGCGGCAAGAACACCGACTGGAG 130
Db 61 AAGCGGAGATCGCGCAGAGACTTGAAGATGTCTTTCAGGGAAGAACACCGATCTTGAG 120

Qy 131 GTGCTGATGGAAGTGGCTGAAGACAGGCGCCCTCTGAGCGCGCTGAGCGCGCGCTTGTG 190
Db 121 GCATCTCATGGAATGGCTTAAAGACAAAGACCAATCTCTGTCATCTGATTAAGGGAATTTA 180

Qy 191 GGCTTGTGTTTCACTTCACTGAGCGCGCGCTGAGCGCGCGCTGAGCGCGCGCTTGTG 250
Db 181 GGATTCGATTCAGCTTCACTGAGCGCGCGCTGAGCGCGCGCTGAGCGCGCTTGTG 240

Qy 251 CAGAACGCTTGAAGAGGAGATCACCTTCCACGCGCGCAAGGAGATCAGGCTGAGCTGAT 310
Db 241 CAAAATGCCCTTGTGGAACCGGAGATCCAAACAAACATGAGCAGAGCAGTAAACCTGTAC 300

Qy 311 AGGAGCTGAAGAGGAGATCACCTTCCACGCGCGCAAGGAGATCAGGCTGAGCTACAGC 370
Db 301 AGGAAGCTTAAAGAGAGAAATAACATTCATGGGGCAAAAGAGGTGGCACTCAGCTATTCC 360

Qy 371 GCCGCGCGCTTGGCAGCTGATGGGCTGTATCTAACAGAGATGGGCGCGCTGAGCACC 430
Db 361 ACTGTTGCACTAGCCAGCTGATGGGCTCATATACAAAGATGGGAACCTGTGACACAC 420

Qy 431 GAGTTGGCTTGGCAGCTGATGGGCTGATGGGCTGATGGGCTGATGGGCTGATGGGCTG 490
Db 421 GAAATGGCAATTTGGCTTGGTATGGCGCACATGTGAACAGATCGCTGATTTCCAGCATCGA 480

Qy 491 AGCCACAGGAGATGGTGTGATGGTGTGATGGTGTGATGGTGTGATGGTGTGATGGTGTG 550
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Db      481  TCTCAGGCGAGTGGTGACAAACCAACCCATTAATCAGACATGAATAACAGAAATGTA 540
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Db      541  TTAGCCAGTACACCGCTAAAGCCATGAGCAGATGGCAGGATCGAGTGAGCAGCAGCA 600
Qy      611  GAGGCCATGGAGTGGCCAGCAGCCAGCAGGAGGAGTGGTGAGGAGGATGAGGAGCAGC 670
Db      601  GAGGCCATGGAGTGGCTAGTAAGGCTAGGCGATGGTTCAGGCAATGAGAACCAATTGG 660
Qy      671  ACCCAACCCAGCAGCAGCCCGCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCCTAC 730
Db      661  ACCCAACCCAGTCTCAGTGGCGGTTGAAGAGATGATCTCTTGAAATTTGAGCCCTAC 720
Qy      731  CAGAGCGCATGGCGCTGCAGATGCAGCGCTTCAAG 766
Db      721  CAGAAACGGATGGGAGTGCAATGCAGCGATTCAAG 756

RESULT 13
US-09-762-861B-3
; Sequence 3, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; CURRENT FILING DATE: 2001-02-13
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-762-861B-3

Query Match      61.6%; Score 477.2; DB 3; Length 756;
Best Local Similarity 76.9%; Pred. No. 1.4e-81;
Matches 581; Conservative 1; Mismatches 174; Indels 0; Gaps 0;

Qy      11  ATGAGCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCGAGCGCCCTTG 70
Db      1  ATGAGTCTTCTGACCGAGGTGAAACGTACGTCTCTCTATCTGATACATCAGGCCCTC 60

Qy      71  AAGGCCGAGATCGCCAGAGGCTGGAGAGCGTGTTCGCGCGCAAGAACACCGACCTGGAG 130
Db      61  AAGGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGAGGGAAGAACACCGATCTTGAG 120

Qy      131  GTGCTGATGGAGTGGCTGAAGACACGAGCCCATCTCTGAGCCCTTGACCAAGGGGATCTG 190
Db      121  GCACCTCATGGAATGGCTAAAGACAAACCAATCTGTCTCTCTATCTGACTTAAAGGGATTTA 180

Qy      191  GGCTTCGTGTTACCTGACCGTCCCGCAGCGCGCGCTGCGAGCCCGCTTCTGTCG 250
Db      181  GGATTCGTATTACGCTCACCCTGCGGAGTGGAGGAGCTGCGAGCGTAGACGCTTTGTC 240

Qy      251  CAGAACGCCCTGAAACGGCAACGGCCACCAACATGGAACAAAGAGGCTGAGCTGTAC 310
Db      241  CAARATGCCCTTAGTGGAAACGGAGATCCAAACACATGGACAGACGATAAACTGTAC 300

Qy      311  AGGAAGCTGAAGAGGGAGATCACTTCCACGCGCCAAAGGAGATCAGCTGAGCTACAGC 370
Db      301  AGGAAGCTTAAAGAGAAATAACATTCATGGGGCAAAAGAGTGGCACTCAGCTATTTC 360
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Qy      371  GCCGCGCCTTGGCCAGCTGCATGGGCTGTATCTTACAACAGAGATGGGCGCGTGACCAACC 430
Db      361  ACTGGTGCATCTAGCCAGCTGCATGGGACTCATATAACAAGAAATGGGAACCTGTGACAAACC 420

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Qy      491  AGCCACAGGCGAGATGGTGACCCACCAACCCCTGATCAGGCGACGAGAACAGATGGTG 550
Db      481  TCTCAGAGGCGAGATGGTGACAAACCAACCCATTAAATCAGACATGAACAGAAATGTA 540

Qy      551  CTGGCCAGCACACCGCCAAAGCCATGAGCAGATGGCCGCGCAGCAGCAGCAGCCGCC 610
Db      541  TTAGCCAGTACACCGCTAAAGCCATGGAGCAGATGGCAGGCTCGAGTGAGCAGCAGCA 600

Qy      611  GAGGCCATGGAGTGGCCAGCAGCCAGGCGCAGATGGTGAGGAGGATGAGGAGCAGCAGC 670
Db      601  GAGGCCATGGAGTGGCTAGTAAGGCTAGGCGATGGTTCAGGCAATGAGAACCAATTGG 660

Qy      671  ACCCAACCCAGCAGCAGCCCGCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCCTAC 730
Db      661  ACCCAACCCAGTCTCAGTGGCGGTTGAAGAGATGATCTCTTGAAATTTGAGGCCCTAC 720

Qy      731  CAGAGCGCATGGCGCTGCAGATGCAGCGCTTCAAG 766
Db      721  CAGAAACGGATGGGAGTGCAATGCAGCGATTCAAG 756

RESULT 14
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; Sequence 3, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-3

Query Match      61.6%; Score 477.2; DB 3; Length 756;
Best Local Similarity 76.9%; Pred. No. 1.4e-81;
Matches 581; Conservative 1; Mismatches 174; Indels 0; Gaps 0;

Qy      11  ATGAGCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCGAGCGCCCTTG 70
Db      1  ATGAGTCTTCTGACCGAGGTGAAACGTACGTCTCTCTATCTGATACATCAGGCCCTC 60

Qy      71  AAGGCCGAGATCGCCAGAGGCTGGAGAGCGTGTTCGCGCGCAAGAACACCGACCTGGAG 130
Db      61  AAGGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGAGGGAAGAACACCGATCTTGAG 120

Qy      131  GTGCTGATGGAGTGGCTGAAGACACGAGCCCATCTCTGAGCCCTTGACCAAGGGGATCTG 190
Db      121  GCACCTCATGGAATGGCTAAAGACAAACCAATCTGTCTCTCTATCTGACTTAAAGGGATTTA 180

Qy      191  GGCTTCGTGTTACCTGACCGTCCCGCAGCGCGCGCTGCGAGCCCGCTTCTGTCG 250
Db      181  GGATTCGTATTACGCTCACCCTGCGGAGTGGAGGAGCTGCGAGCGTAGACGCTTTGTC 240

Qy      251  CAGAACGCCCTGAAACGGCAACGGCCACCAACATGGAACAAAGAGGCTGAGCTGTAC 310
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Db 241 CAAATGCCCTTAGTGGAAACGGAGATCCAAACACATGGACAGAGCAGTAAACTGTAC 300
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Qy 371 GCGGGCCCTGGCCAGCTGCATGGGCTGTATCTACAAAGGATGGGGCGGTGACCAACC 430
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Qy 431 GAGGTGCTTCCGCTGTGTGGCCACCTGCAGCAGATCGCCGACAGCCAGCACCGC 490
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Qy 491 AGCCACAGGAGATGGTGACCAACCAACCCCTGTATCAGGCACGAGAACAGGATGGTG 550
Db 481 TCTCAGAGGAGATGGTGACNAACCAACCCATTAATCAGACATGAANACAGNATGGTA 540
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Db 541 TTAGCCAGTACACCGCTTAAAGCCATGGAGCAGATGGCAGGTCGAGTGAGCAGGCAGCA 600
Qy 611 GAGCCATGGAGTGGCCAGCCAGCCAGCAGCAGATGGTGAGGSCCATGAGAACCATCGC 670
Db 601 GAGCCATGGAGTGGTGTAGTAAGGCTAGGCGATGGTRCAGGCAATGAGAAACCATTTGG 660
Qy 671 ACCCAGCCAGCAGCAGCGCGCTGAAGAACACCTGTGGAGAACCTGCAGGCCCTAC 730
Db 661 ACCCAGCTAGCTCAGTGCCGCTTGAAGATGATCTCTTGAATTTGACGGCTTAC 720
Qy 731 CAGAAAGCGCATGGCGTGCAGATCGAGCGCTTCAAG 766
Db 721 CAGAAACGGATGGGAGTGCAATGCAGCGATTCAAG 756

RESULT 15

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; Sequence 3, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-CL-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-434-811A-3

Query Match 61.6%; Score 477.2; DB 3; Length 756;
Best Local Similarity 76.9%; Pred. No. 1.4e-81;
Matches 581; Conservative 1; Mismatches 174; Indels 0; Gaps 0;

Qy 11 ATGAGCCTGTGACCGAGGTGGAGACCTACGTGTGACGATCATCCCCAGCGGCCCTTG 70
Db 1 ATGAGTCTTCTGACCGAGGTGGAACGTACGTCTCTATCGTACCATCAGGCCCCCTC 60
Qy 71 AAGGCCGAGATCGCCAGGAGGTGGAGGACGTGTTCGCGGCAAGAACACCGACCTGGAG 130
Db 61 AAAGCCGAGATCGCCAGGACTTGAAGATGCTTTGAGGGAGAGAACACCGATCTTGAG 120

Qy 131 GTCTGTAGTGAGTGGCTGAAGACAGCGCCCATCTGAGCCCTGACCAAGGCGATCCTG 190
Db 121 GCACCTATGGAATGGCTTAAAGACAGACCAATCTGTCACTCTGACTTAAGGATTTTA 180
Qy 191 GCGTTCGTGTTCAACCTGTGACCGTCCAGCGCGCGCTGCGAGCGCCCGCTTTCGTG 250
Db 181 GGATTGTGATTACGCTCACCGTCCAGTGGAGGAGCTGCGAGCGTACAGCTTTGTC 240
Qy 251 CAGAAAGCCCTGAAACGGCGAACCGCGACCCCAACAAATGAGCAAGGCCGTGAAGCTGTAC 310
Db 241 CAAATATGCCCTTAGTGGAAACGGAGATCCAAACAAATGACAGAGCAGTAAACCTGTAC 300
Qy 311 AGGAAGCTGAAGAGGAGATCACCTTCCAGCGCGCAAGGAGATCAGCCTGAGCTACAGC 370
Db 301 AGGAAGCTTAAAGAGAAATAACATTCATGGGGCAAAAGAGGTGGCACTCAGCTATTCC 360
Qy 371 GCGGGGCCCTGCGCCAGCTGTGATGGGCTGTATCTACAAAGGATGGGCGCGCTGACCAACC 430
Db 361 ACTGGTGCACTAGCCAGCTGCATGGGACTCATATACACAGNATGGGAACTGTGACAACC 420
Qy 431 GAGGTGCGCTTTCGGCCTGTGTGCGCACCTGCGAGCAGATCGCCGACAGCCAGCACCGC 490
Db 421 GAAAGTGGCATTTGGCCTGTGTATGCGCCACATGTGTGAACAGATCGCTGATTTCCAGCATCGA 480
Qy 491 AGCCACAGGCGAGATGGTGACCAACCAACCCCTGTATCAGGCACGAGAACAGATGGTG 550
Db 481 TCTCAGAGGCGAGATGGTGACAAACCAACCCCATTAATCAGACATGAANACAGNATGGTA 540
Qy 551 CTGCGCAGCACACCGCCAAAGGCCATGGAGCAGATGGCCGCGCAGCAGCAGCGCGCC 610
Db 541 TTAGCCAGTACACCGCTTAAAGCCATGGAGCAGATGGCAGGTCGAGTGAGCAGGCAGCA 600
Qy 611 GAGGCCATGGAGTGGCCAGCCAGCGCAGCAGATGGTGAGGCGCATGAGGACCATCGGC 670
Db 601 GAGGCCATGGAGTGTCTAGTAAGGCTAGGCGATGGTRCAGGCAATGAGAACCATTTGG 660
Qy 671 ACCCAGCCAGCAGCGCGCTGAAGAACGACCTGTGGAGAACCTGCAGGCCCTAC 730
Db 661 ACCCAGCTAGCTCAGTGCCGCTTGAAGATGATCTCTTGAATTTGACGGCTTAC 720
Qy 731 CAGAAAGCGCATGGCGTGCAGATCGAGCGCTTCAAG 766
Db 721 CAGAAACGGATGGGAGTGCAATGCAGCGATTCAAG 756

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GenCore version 5.1.7
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Total number of hits satisfying chosen parameters: 19587084

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	498.8	64.4	774	8	US-10-729-830-1
7	497	64.1	985	8	US-10-866-484-9
8	489.4	63.1	1027	6	US-10-177-390-31
9	487.4	62.9	1023	6	US-10-065-133A-1
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25 477.2 61.6 756 8 US-10-872-014-3 Sequence 3, Appli

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27 474.6 61.2 1002 7 US-10-435-723A-3 Sequence 3, Appli

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32 473.4 61.1 1027 7 US-10-381-530-7 Sequence 7, Appli

33 472.6 61.0 759 8 US-10-617-569-3 Sequence 3, Appli

34 77.6 10.0 1092 6 US-10-138-098-13 Sequence 13, Appli

35 77.6 10.0 1092 8 US-10-476-615-13 Sequence 13, Appli

36 77.6 10.0 3020 6 US-10-138-098-21 Sequence 21, Appli

37 77.6 10.0 3020 8 US-10-476-615-21 Sequence 21, Appli

38 77.6 10.0 3021 6 US-10-138-098-22 Sequence 22, Appli

39 77.6 10.0 3021 6 US-10-138-098-23 Sequence 23, Appli

40 77.6 10.0 3021 6 US-10-138-098-24 Sequence 24, Appli

41 77.6 10.0 3021 8 US-10-476-615-22 Sequence 22, Appli

42 77.6 10.0 3021 8 US-10-476-615-23 Sequence 23, Appli

43 77.6 10.0 3021 8 US-10-476-615-24 Sequence 24, Appli

44 77 9.9 1377 8 US-10-411-910A-266 Sequence 266, App

45 76.2 9.8 1725 8 US-10-411-910A-196 Sequence 196, App

ALIGNMENTS

RESULT 1

US-10-729-830-3

; Sequence 3, Application US/10729830

; Publication No. US20050032730A1

; GENERAL INFORMATION:

; APPLICANT: Von der Muelbe, Florian

; APPLICANT: Hoerk, Ingmar

; APPLICANT: Pascolo, Steve

; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA

; FILE REFERENCE: 2793-1-001PCT/CIP

; CURRENT APPLICATION NUMBER: US/10/729,830

; CURRENT FILING DATE: 2003-12-05

; PRIOR APPLICATION NUMBER: PCT/EP02/06180

; PRIOR FILING DATE: 2002-06-05

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; TYPE: DNA

; LENGTH: 775

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Influenza

; OTHER INFORMATION: matrix: gene with increased G/C-content

; FEATURE:

; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop

; OTHER INFORMATION: codon: tga (nucleotides 767 to 769)

US-10-729-830-3

Query Match 100.0%; Score 775; DB 8; Length 775;

Best Local Similarity 100.0%; Pred. No. 8.3e-175; Indels 0; Gaps 0;

Matches 775; Conservative 0; Mismatches 0;

Qy 1 AGATCTAAAGATGAGCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60

Db 1 AGATCTAAAGATGAGCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG 60

Qy 61 CGGCCCCCTGAAGGGCCGAGATCCGCCAGAGCGTGGAGGAGCGTTCGCCCGGCAAGACAC 120

Db 61 CGGCCCCCTGAAGGGCCGAGATCCGCCAGAGCGTGGAGGAGCGTTCGCCCGGCAAGACAC 120

Qy 121 CGACCTGGAGGTGCTGATGGAGTGGTGAAGCCAGCCCATCTGAGCCCCCTGACCAA 180

Db 121 CGACCTGGAGGTGCTGATGGAGTGGTGAAGCCAGCCCATCTGAGCCCCCTGACCAA 180

Qy 181 GGGCATCTGGGCTTCGTGTTACCTGACCGTCCCGAGCGCGGCTGCGACGCCG 240

Db 181 GGGCATCTGGGCTTCGTGTTACCTTACCTGACCGTCCAGCGAGCGCGCTGACGCGCG 240
Qy 241 CCGCTTCGTGAGAAAGCCCTGAAACGCGCAACGCGGACCCCAACAAATGACAAAGGCGGT 300
Db 241 CCGCTTCGTGAGAAAGCCCTGAAACGCGCAACGCGGACCCCAACAAATGACAAAGGCGGT 300
Qy 301 GAAGCTGTACAGGAAGCTGAAGAGGAGATCACCTTCCAGCGGCCCAAGGAGATCACCT 360
Db 301 GAAGCTGTACAGGAAGCTGAAGAGGAGATCACCTTCCAGCGGCCCAAGGAGATCACCT 360
Qy 361 GAGCTACAGCGCGCGCGCTTGGCCAGCTGATGGGCTGTATCTACAAAGGATGGCGC 420
Db 361 GAGCTACAGCGCGCGCGCTTGGCCAGCTGATGGGCTGTATCTACAAAGGATGGCGC 420
Qy 421 CGTGACCAACGAGGTGGCTTCGGCTTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 480
Db 421 CGTGACCAACGAGGTGGCTTCGGCTTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 480
Qy 481 CCAGCAGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 540
Db 481 CCAGCAGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 540
Qy 541 CAGATGGTGTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 600
Db 541 CAGATGGTGTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 600
Qy 601 GCAGGCGCGGAGGCGCAGGAGTGCGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 660
Db 601 GCAGGCGCGGAGGCGCAGGAGTGCGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 660
Qy 661 GACCATCGGCACCCACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 720
Db 661 GACCATCGGCACCCACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 720
Qy 721 GCAGGCTTACAGAAAGCGCATGGGCGTGCAGATGAGCGCTTCAAGTGAAGTACT 775
Db 721 GCAGGCTTACAGAAAGCGCATGGGCGTGCAGATGAGCGCTTCAAGTGAAGTACT 775

RESULT 2
US-10-729-830-6
; Sequence 6, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 942
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA with increased G/C-content and
; OTHER INFORMATION: stabilisation sequences
; FEATURE:
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
; OTHER INFORMATION: respectively.
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
; OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-6

Query Match 100.0%; Score 775; DB 8; Length 942;
Best Local Similarity 87.7%; Pred. No. 8.3e-175;
Matches 680; Conservative 95; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGATCTAAGATGAGCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATATCCCCAG 60
Db 46 AGAUCUAAAGUAGGCGGUGGAGACCUACGUGGUGGAGACCUACGUGGUGGAGCAUCCCCAG 105
Qy 61 CGGCCCCCTCAAGGCGCGAGATCGCCAGAGGCTGGAGAGCTGTTCGCCGCGCAAGAACAC 120
Db 106 CGGCCCCCTCAAGGCGCGAGUCCGCCAGAGCGUGGAGGACGUGUUCGCCGCGCAAGAACAC 165
Qy 121 CGACTGTGAGGTGCTGATGAGTGGTGAAGACAGGCGCCATCTCTGAGCCCCCTGACCAA 180
Db 166 CGACCCUGAGGUGUGAUGGAGUGGUGGUGAAGACAGGCGCCAUCCUGAGCCCCCUGAGCAA 225
Qy 181 GGGCATCTGGGCTTCGTGTTACCTTACCTGACCGTGGCGGCGGCGCGCTGACGCGCG 240
Db 226 GGGCAUCCUGGGGCUUGUGUUCACCCUGACCGGCGCGGCGGCGCGCGCGCGCGCG 285
Qy 241 CCGCTTCGTGAGAAAGCCCTTGAACGCGCAACGCGGACCCCAACAAATGACAAAGGCGGT 300
Db 286 CCGCUUCUGGAGGAGACGCGCCUGAAGCGGCAACGCGGACCCCAACAAAGGCGCGG 345
Qy 301 GAAGCTGTACAGGAAGCTGAAGAGGAGATCACTTCCAGCGCGCCCAAGGAGATCAGCCT 360
Db 346 GAAGCUGUACAGGAAGCUGAAGAGGAGAGUACCUUCCAGCGGCGCCAAAGGAGATCAGCCU 405
Qy 361 GAGCTACAGCGCGCGCGCTTGGCGCAGCTGCATGGGCGCTGATCTACAAAGGATGGCGC 420
Db 406 GAGCUACAGCGCGCGCGCCUUGGCGCAGCUGGCGGCGGCGGCGGCGGCGGCGGCG 465
Qy 421 CGTGACCAACGAGGTGGCTTCGGCTTCGTGCGCCACCTGCGGAGCAGATCGCGGACAG 480
Db 466 CGUGACCAACGAGGUGGCGCUUCGCGCUGGUGGCGCCACCGGAGCAGAUCCCGGACAG 525
Qy 481 CCAGCAGCGCAGCCACAGGAGATGTTGACCAACAAACCCCTGATCAGGCGACGAGAA 540
Db 526 CCAGCAGCGCAGCCACAGGAGAGUUGGAGACCAACCAACCCCGGCGGCGGCGGCGGAGAA 585
Qy 541 CAGGATGGTGTGGCGCAGCACCGCCCAAGGCCATGAGCAGATGCGCGGCGGCGGCGG 600
Db 586 CAGGAUGGUGUGGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 645
Qy 601 GCAGGCGCGCGGCGCATGAGGTGGCGCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
Db 646 GCAGGCGCGCGGCGCAUGGAGGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 705
Qy 661 GACCATCGGCACCCACCCAGCAGCAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
Db 706 GACCAUGGCGCACCCACCCAGCAGCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 765
Qy 721 GCAGGCTTACAGAAAGCGCATGGGCGTGCAGATGCGCGCTTCAAGTGAAGTACT 775
Db 766 GCAGGCGCAACAGAAAGCGCAUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 820

RESULT 3
US-10-729-830-4
; Sequence 4, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
US-10-729-830-4

	; NUMBER OF SEQ ID NOS: 13	
	; SOFTWARE: PatentIn Ver. 2.1	
	; SEQ ID NO 4	
	; LENGTH: 844	
	; TYPE: DNA	
	; ORGANISM: Artificial Sequence	
	; FEATURE:	
	; OTHER INFORMATION: Description of Artificial Sequence: Influenza	
	; OTHER INFORMATION: matrix: gene for secreted form (with N-terminal	
	; OTHER INFORMATION: signal sequence) with increased G/C-content	
	; FEATURE:	
	; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop	
	; OTHER INFORMATION: codon: tga (nucleotides 836 to 838)	
	US-10-729-830-4	
	Query Match 98.3%; Score 762; DB 8; Length 844;	
	Best Local Similarity 100.0%; Pred.No. 1e-171;	
	Matches 762; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
Qy	14 AGCCTGCTGACCGAGGTGGAGACTTACGTGTGTGAGCATATCCCGAGGCCGCCCTGAAG	73
Db	83 AGCCTGCTGACCGAGGTGGAGACTTACGTGTGTGAGCATATCCCGAGGCCGCCCTGAAG	142
Qy	74 GCCGAGATGCCCAAGAGCTGGAGAGCTGTTCCCGCGAAGAACACCAGACTGGAGGTG	133
Db	143 GCCGAGATGCCCAAGAGCTGGAGAGCTGTTCCCGCGAAGAACACCAGACTGGAGGTG	202
Qy	134 CTGATGAGTGCTTGAAGACACAGGCCCATCTCTGAGCCCCCTGACCAAGGGCATCTCGGC	193
Db	203 CTGATGAGTGCTTGAAGACACAGGCCCATCTCTGAGCCCCCTGACCAAGGGCATCTCGGC	262
Qy	194 TTGCTGTTACCTGACCGTCCACAGGAGCGCGGCTGTGACGCGCGCGCTTCGTGCGAG	253
Db	263 TTGCTGTTACCTGACCGTCCACAGGAGCGCGGCTGTGACGCGCGCGCTTCGTGCGAG	322
Qy	254 AACGCCCTGAACGGCAACGGCGACCCCAAACAATGGAACAAGGCGTGAAGCTGTACAGG	313
Db	323 AACGCCCTGAACGGCAACGGCGACCCCAAACAATGGAACAAGGCGTGAAGCTGTACAGG	382
Qy	314 AAGCTGAAGAGGGAGATCACCTTCCAGCGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC	373
Db	383 AAGCTGAAGAGGGAGATCACCTTCCAGCGCGCCAAGGAGATCAGCCTGAGCTACAGCGCC	442
Qy	374 GGCGCCCTGGCAGCTGTATGGGCTGTATCTACAAACAGGATGGGCGCGCTGACCAACCGAG	433
Db	443 GGCGCCCTGGCAGCTGTATGGGCTGTATCTACAAACAGGATGGGCGCGCTGACCAACCGAG	502
Qy	434 GTGCGCTTCGGCCCTGGTGTGGCCACCTGCGAGCAGATCGCCGACAGCACCGCAGC	493
Db	503 GTGCGCTTCGGCCCTGGTGTGGCCACCTGCGAGCAGATCGCCGACAGCACCGCAGC	562
Qy	494 CACAGGCAGATGGTGACCAACACACCCCCTGATCAGGCACGAGAA CAGGATGGTGTG	553
Db	563 CACAGGCAGATGGTGACCAACACACCCCCTGATCAGGCACGAGAA CAGGATGGTGTG	622
Qy	554 GCCAGCAACCCGCAAGGCCATGGAGCAGATGGCGCGCAGCAGCGCCGCCCGAG	613
Db	623 GCCAGCAACCCGCAAGGCCATGGAGCAGATGGCGCGCAGCAGCGCCGCCCGAG	682
Qy	614 GCCATGAGGTGGCCAGCCAGCGCAGATGGTTCAGGCGCATGAGGACCATCGGCACC	673
Db	683 GCCATGAGGTGGCCAGCCAGCGCAGATGGTTCAGGCGCATGAGGACCATCGGCACC	742
Qy	674 CACCCAGCAGCAGCGCGGCTTGAAGAAGACCTGTCTGGAGAACTCTCAGCGCTTACCAG	733
Db	743 CACCCAGCAGCAGCGCGGCTTGAAGAAGACCTGTCTGGAGAACTCTCAGCGCTTACCAG	802
Qy	734 AAGCGCATGGCGTGCAGATGCAGCGCTTAAGTGAAC TAGT	775
Db	803 AAGCGCATGGCGTGCAGATGCAGCGCTTCAAGTGAAC TAGT	844

RESULT 4

614	Qy	GCCATGGAGTGGCCAGCCAGCCAGGCAGATGGTGCAGGCCCATGAGGACCATCGGCACC	673
728	Db	GCCATGGAGTGGCCAGCCAGCCAGGCAGATGGTGCAGGCCCATGAGGACCATCGGCACC	787
674	Qy	CACCCAGCAGAGCGCCGCGCTGAAGAACGACCTGCTCGAGAACCTGCGAGCGCTACCGAG	733
788	Db	CACCCAGCAGAGCGCCGCGCTGAAGAACGACCTGCTCGAGAACCTGCGAGCGCTACCGAG	847
734	Qy	AAGGCGATGGGGTTCAGATGCGAGCGCTTCAAGTGAACTAGT	775
848	Db	AAGGCGATGGGGTTCAGATGCGAGCGCTTCAAGTGAACTAGT	889

```

RESULT 5
US-10-729-830-5
; Sequence 5, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: Optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 942
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA with stabilisation sequences
; FEATURE:
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
; OTHER INFORMATION: respectively.
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
; OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
; US-10-729-830-5

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361	Qy	GAGCTACAGCGCCGGCGCCCTGGCCACGCTGCATGGGCTGATCTACAACAGAGTGGGCGC	420
406	Db	CAGTUAUUCUGCUGGUGCACTUGGCGAGTUGUAUGGGCCUCAUAUACAAACAGGAUUGGGGCGC	465
421	Qy	CGTGACCACCGAGGTGGCCCTTTGGCCCTGGTGTGCGCCACCTGCGAGCAGATGCGCCGACAG	480
466	Db	UGUGACCACCUAGAGGUGCAUUUGCCUGGUAUGUGCAACCCUGUGAACAGAUUUGCUGACUC	525
481	Qy	CCAGCACCGGACGCCACAGGCAGATGTGTGACCAACCACCAACCCCTCTGATCAGGCACGAGAA	540
526	Db	CCAGCAUGGUCUACUAGGCCAAUUGGUGACAAACCAACCCACUAAUCAGACACUAGAGAA	585
541	Qy	CAGGATGGTGTGTCGCCAGACCAACGCCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA	600
586	Db	CAGAAUGGUTUUAAGCCAGCACUACAGCVAAGGCUUAUGGAGCAAAUUGGCGUGAUCAGAGUA	645
601	Qy	GCAGGCCCGGAGCGCATGGAGGTGGCCAGCCAGGCCAGGACAGATGGTGCAGGCCCATGAG	660
646	Db	GCAAGCAGCAGAGGCCCAUGGAGGUYUGUAGUCAGCGCAGGCAAAUUGGUGCAAGCGAUGAG	705
661	Qy	GACCATCGGCACCCACCCACGACGACGCGCCGGGCTCTGAAGAACCAACCTGTCTGGAGAACT	720
706	Db	AACCAUUGGAGNACUACCUAGCTCCAGUGCUGGUCUAGAAAAAUAUGAUCUUCUUGAAAAUUU	765
721	Qy	GCAGGCCTTACAGAAAGCGCATGGGGCGTGAGATGCAGCGCTTCAAGTGAATAGT	775
766	Db	GCAGGCCUACUAGAAAAACGAUUGGGGUGCAGUAGCAACGGUUCUAGUGAACUAGU	820

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RESULT 6
US-10-729-830-1
; Sequence 1, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: Optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/Cip
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Influenza virus
; FEATURE:
; OTHER INFORMATION: Influenza matrix: wildtype gene (for comparison)
; FEATURE:
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
; OTHER INFORMATION: codon: tga (nucleotides 767 to 769 )
US-10-729-830-1

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Query Match	64.5%	Score 499.8	DB 8	Length 942
Best Local Similarity	65.5%	Pred. No. 2.4e-109		
Matches 508	Conservative 95	Mismatches 172	Indels 0	Gaps 0
QY	1	AGATCTAAAGATGAGCCTGCTGACCGAGGTGAGACCTACGTGTGAGCATCATCCCCAG	60	
Db	46	AGAUCAAAGAUGAGUCUUUAACCCGAGUGGAAACGACUGUUCUCUUAUCAUCCCCUC	105	
QY	61	CGGCCCTTGAAGGCCGAGATCGCCCCAGAGGCTGGAGACGTGTTCGCGGCAAGAAC	120	
Db	106	AGGCCCCCUCAAGCCGAGAUCCACAGACAGUUAAGAUGUUUGCAGGAGAAACAC	165	
QY	121	CGACTGTGAGGTGTGATGGAGTGTGCTGAAGACCAAGGCCCATCTCTGAGCCCTTGACAA	180	
Db	166	CGAUUCUAGGGUUCUAUGGAAUGGCUAAGACAAGACCAUCCUGUACCUUCUGACUAA	225	
QY	181	GGGCATCTGGGCTTCGTGTTTCACCTGACCTGCCAGCGAGCGGGCCTTGACGGCGG	240	
Db	226	GGGGAAUUAAGAUUUUGUUAUACGCUACCGUGCCCAUGAGCGAGAGACUGACGGUAG	285	
QY	241	CCGCTTCGTGCAGAAACGGCCCTTGAACGGCAAACGGCGACCCCAACAACATGTGAAAGGCCGT	300	
Db	286	ACGCUUUGCCAAAUAGCCCUUAUUGGNAACGGGGAUCCAAUAACAUAGCAAGCAGU	345	
QY	301	GAAGCTGTACAGGAAGCTGAAGAGGAGATCATCTTTCACCGCGCCAAAGGAGATCAGCCT	360	
Db	346	UAAACUGUAAGAAAGCUCACAGAGGAGAAUACAUTUUAUGGGGCCAAAGAAAUUCUACU	405	

Qy 181 GGGCATCTTGGGCTTCTGTTTCAACCTGACCGTCCAGCGAGCGCGGCTTGCAGCGCG 240
Db |||||
Qy 181 GGGGATTTTAGGATTTGTTTCAACCTGACCGTCCAGCGAGCGCGGCTTGCAGCGTAG 240
Db |||||
Qy 241 CCGCTTCGTGAGAACGCGCTTGAACGCGCAACGCGGACCCCAACATGGAACAAGCGGT 300
Db |||||
Qy 241 ACGCTTTGTCAAATGCGCTTAATGGGAACGGGATCCAAATTAACATGGAACAAGCAGT 300
Db |||||
Qy 301 GAAGCTGTACAGGAAGCTGAGAGGGAGATCAACCTTCCACGGCGCCAGGAGATCAGCCT 360
Db |||||
Qy 301 TAAACTGTATAGGAAGCTCAAGAGGGAGATTAACATTCATGGGCGCCAAAGAAATCTCACT 360
Db |||||
Qy 361 GAGCTACAGCGCGCGCGCTTGGCGAGCTGATGGGCTGATCTACAAACAGGATGGGCGC 420
Db |||||
Qy 361 CAGTTATTCTGCTGGTCACTTGGCAGTTGTATGGGCTCATATACAAACAGGATGGGCGC 420
Db |||||
Qy 421 CGTGACCAACGAGGTGGCTTGGGCTTGGGCTGATGGGCGCACTTGCAGAGCATGCGCGACAG 480
Db |||||
Qy 421 TGTGACCACTGAAGTGGCATTTGGCTGTATGTGCAACCTGTGAACAGATTGCTGACTC 480
Db |||||
Qy 481 CCAGACCGACGACGAGGAGATGTTGACCAACCAACCCCTGATCAGGACGAGAA 540
Db |||||
Qy 481 CCAGATCGGTCTCATAGGCAAAATGGTGACAAACCAACCACTAATCAGACATGAGAA 540
Db |||||
Qy 541 CAGGATGGTGTGGCGACACACCGCCAGGCGCATGGAGCAGATGGCGCGCAGCAGCA 600
Db |||||
Qy 541 CAGAAATGGTTTTAGCCAGCATCTACAGCTAAGGCTATGGAGCAATGGCTGATCGAGTGA 600
Db |||||
Qy 601 GCAGGCGCGCAGGCGCATGAGGTGGCGAGCGAGCGGCGAGGCGAGATGTTGCGAGGCGCATGAG 660
Db |||||
Qy 601 GCAAGCAGCAGAGGCGCATGAGGTGGCTGTAGTCAGGCTAGGCAATGGTGAAGCGATGAG 660
Db |||||
Qy 661 GACCATGGGACCCACCGACGAGCGCGCGGCTGAGAAACACCTGCTGGAGAACCT 720
Db |||||
Qy 721 GCAGGCTTACAGAAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAACCTAG 774
Db |||||
Qy 721 GCAGGCTTACAGAAAGCGATGGGCGTGCAGATGCAGCGCTTCAAGTGAACCTAG 774
Db |||||

RESULT 7
US-10-866-484-9
; Sequence 9, Application US/10866484
; Publication No. US20050013826A1
; GENERAL INFORMATION:
; APPLICANT: Shneider, M.
; TITLE OF INVENTION: Vaccine Compositions and Methods
; FILE REFERENCE: 25955-003CIP
; CURRENT APPLICATION NUMBER: US/10/866,484
; CURRENT FILING DATE: 2004-06-11
; PRIOR APPLICATION NUMBER: 60/435,500
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 10/741,466
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 986
; TYPE: DNA
; ORGANISM: Influenza A virus
US-10-866-484-9

Query Match 64.1%; Score 497; DB 8; Length 986;
Best Local Similarity 78.3%; Pred. No. 1.1e-108;
Matches 596; Conservative 0; Mismatches 165; Indels 0; Gaps 0;
Qy 11 ATGAGCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCGAGCGGCGCCCTG 70
Db |||||
Qy 1 ATGAGCTGCTTCAACCGAGGTGCAAAACGTACGTTCTCTCTATCGTCCCGTCAGGCGCCCTC 60
Db |||||

Qy 71 AAGCCCGAGATCGCCAGAGGCTGGAGGACGTGTTCGCCGCAAGAAACACCGACCTGGAG 130
Db |||||
Qy 61 AAGCCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCTGGGAAGAAACACCGATCTCGAG 120
Db |||||
Qy 131 GTGCTGATGAGTGGCTGAAGACGAGCGCCCATCTCTAGCGCCCTTGCACCAAGGGCATCTCG 190
Db |||||
Qy 121 GCATCTATGGAATGGCTTAAAGACAAGACCAATCTCTGTCATCTGACTTAAGGGGATTTTA 180
Db |||||
Qy 191 GGCCTTCTGTTTACCTGACCGTCCAGCGAGGCGCGCTTGCAGCGCGCGCTTCTGTCG 250
Db |||||
Qy 181 GGATTTGTTTCACTGCTTCACTGCGGCTGAGGCGAGGACTGCGAGCTGAGACGCTTGTGTC 240
Db |||||
Qy 251 CAGAACCCCTTGAACGCGCAACGCGACCCCAACAAATGGAACAAAGCGCTGAAGCTGTAC 310
Db |||||
Qy 241 CAGAAATGCCCTTAATGGGAATGGGATCCAAACAAATGAGACGGGCGAGTGAATCTGTAC 300
Db |||||
Qy 311 AGGAAGCTGAAGAGGGAGATCAGCTTCCAGCGGCGCAAGGAGATCAGGCTGAGCTACAGC 370
Db |||||
Qy 301 AGGAAGCTCAAAAGGGAAATTTACATTTCCAGGGGCGCAAGAAAGTAGCGCTCAGTTATTCT 360
Db |||||
Qy 371 GCGGCGCGCTTGGCGCAGCTGATGGGCTGTATCTACAAACAGATGGGCGCGTGAACACC 430
Db |||||
Qy 361 ACTGTCGACTTGGCGCAGCTGATGGGCTCATATACAAACAGATGGGCGCTGTAAACCACT 420
Db |||||
Qy 431 GAGGTGGCTTGGCGCTTGGCGCAGCTTGCAGCAGATTCGCCGAGCAGATTCGCCGAGCAGC 490
Db |||||
Qy 421 GAAGTGGCATTTGGGCTAGTGTGTCACATTTGTGAGCAGATTCGCCGACTCCAGCATCGG 480
Db |||||
Qy 491 AGCCACAGGCGAGTGTGACCAACCAACCCCTGTATCAGGCGACGAGAACAGGATGGTG 550
Db |||||
Qy 481 TCCACACAGCAGATGGTGACGACCAACCAACCCCTAATACAGATGAGAACAGGATGGTG 540
Db |||||
Qy 551 CTGCGCAGCAGCAGCGCAAGGCGCATGAGCAGATGGCGCGCAGCAGCAGCAGCGCGCC 610
Db |||||
Qy 541 CTGCGCAGTACCAAGGCTAAGGCGCATGAGCAGATGGCAGGCTCGAGTGAACAGCAGCA 600
Db |||||
Qy 611 GAGGCCATGAGGAGTGGCGCAGCGCAGGCGCAGATGGTGCAGGCGCATGAGGAGCAGCATCGGC 670
Db |||||
Qy 601 GAAGCCATGAGGAGTGGCTAGTCAAGCTAGGCGATGGTGCAGGCGCATGAGGAGCAGCATCGGC 660
Db |||||
Qy 671 ACCCAGCCAGCAGCAGCGCGCGCTGAGAACGACCTGCTGGAGAACCTGCGAGCGCTTAC 730
Db |||||
Qy 661 ACTCAGCTAGCTCCAGTGGCGGCTTAAAGATGATCTTCTTGAATAATTTGAGGCGCTTAC 720
Db |||||
Qy 731 CAGAAAGCGATGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
Db |||||
Qy 721 CAGAAACGATGGGAGTGCAATGCAGCGATTTCAAGTGATC 761
Db |||||

RESULT 8
US-10-177-390-31
; Sequence 31, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Influenza virus
US-10-177-390-31

Query Match 63.1%; Score 489.4; DB 6; Length 1027;
Best Local Similarity 77.2%; Pred. No. 7.3e-107;
Matches 595; Conservative 0; Mismatches 176; Indels 0; Gaps 0;


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1 // GENERAL INFORMATION:
2 // APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
3 // APPLICANT: Education
4 // APPLICANT: Dowling, Patricia W.
5 // APPLICANT: Youngner, Julius S.
6 // TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
7 // FILE REFERENCE: EQ-1-CI-PUS-1
8 // CURRENT APPLICATION NUMBER: US/10/434,811A
9 // CURRENT FILING DATE: 2003-05-08
10 // PRIOR APPLICATION NUMBER: PCT/US99/18583
11 // PRIOR FILING DATE: 1999-08-12
12 // PRIOR APPLICATION NUMBER: 09/133,921
13 // PRIOR FILING DATE: 1998-08-13
14 // NUMBER OF SEQ ID NOS: 43
15 // SOFTWARE: PatentIn version 3.1
16 // SEQ ID NO 1
17 // LENGTH: 1023
18 // TYPE: DNA
19 // ORGANISM: Equine influenza virus H3N8
20 // FEATURE:
21 // NAME/KEY: CDS
22 // LOCATION: (25)..(780)
23 // OTHER INFORMATION:
24 // FEATURE:
25 // NAME/KEY: misc feature
26 // LOCATION: (663)..(663)
27 // OTHER INFORMATION: At nucleotide 663, r = a or g
28 // OTHER INFORMATION: At amino acid residue 213, Xaa = Val
29 // US-10-434-811A-1

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Query Match	62.9%	Score 487.4	DB 7	Length 1023
Best Local Similarity	76.9%	Pred. No. 2.2e-106		
Matches 593	Conservative 1	Mismatches 177	Indels 0	Gaps 0
QY	1	AGATCTAAAGATGAGCCTGCTTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAG	60	
DB	15	ATATTTAAAGATGAGTCTTCTGACCGAGGTGCTAAACGTACGTTCTCTATCTGATCCATC	74	
QY	61	CGGCCCCCTGAAGGCCGAGATCGCCCCAGAGGCTGGAGACGTTGTCGCCGGCAAGAAC	120	
DB	75	AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTTGAAGATGCTCTTTGCGAGGAAGAAC	134	
QY	121	CGACCTGGAGGTGCTGATGGATGGCTGTGAAGACCAAGGCCCATCTGAGCCCCCTGACCA	180	
DB	135	CGATCTTTGGGCACTCATATGGAATGGCTTAAGACAAGACCAATCTGTCACTCTGACTAA	194	
QY	181	GGGCATCCTGGGCCTTCGTGTTTCACTGACCGCTGCCAGCGCGCGCCCTGACGCGCG	240	
DB	195	AGGGATTTTAGGATTCGTATTACGCTCACCGTGCCTCAGTGGCGAGGACTGCGCGTAG	254	
QY	241	CCGCTTCGTGCAGAACGCCCTTGAAACGGCAACGGCGCAACCCCAACAATGGACAAGCCGT	300	
DB	255	ACGCTTTGTCCAAATGCGCCTTAGTGAAACGGAGATCCAAACAACATGGACAGAGCAGT	314	
QY	301	GAAGCTCTACAGGAAGCTGAAGAGGGAGATCACTTCCACGGCGCCAGGAGATCAGCCT	360	
DB	315	AAAACTGTACAGGAAGCTTAAAGAGAAATAACATTCCTGGGGCAAAAGAGTGGCACT	374	
QY	361	GAGCTACAGCGCCGGCGCCCTGGCCAGCTGATGGCCCTGATCTACAAACAGGATGGGCGC	420	
DB	375	CAGCTATTCACATCGTGCACTAGCCAGCTGATGGGACTCATATACACAGAAATGGGAAC	434	
QY	421	CGTGACCAACCGAGGTGGCCTTCGGCCTGGTGTGGCCCACTTGGGAGCAGATCGCCGACG	480	
DB	435	TGTGACAACCGAAGTGGCAATTTGGCCCTGGTATGGCCCACTGTGAACAGATCGCTGATTC	494	
QY	481	CCAGCACCGCAGCCACAGGCAGATGGTGACCAACCAACCCCTGTGATCAGGCACGAA	540	
DB	495	CCAGCATCGATCTCACAGGCAGATGGTGACAACCAACCCATTTAATCAGACATGAANA	554	
QY	541	CAGGATGGTGTGGCCAGCAACCAACCGCAAGGCCATGGAGCAGATGGCCGGGACGACGA	600	
DB	555	CAGAAATGGTATTAGCCAGTACCAACGGCTAAAGCCATGGAGCAGATGGCAGGCTCAGTGTA	614	

Qy	601	GCAGGCGCCGAGGCCATGAGGTGGCCAGCCAGGCCAGAGATGGTCAGGCCCATGAG	660
Db	615	GCAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTRCAGGCCAATGAG	674
Qy	661	GACCATCGGACCCACCCAGCAGCAGCGCCGGCTGAAGAACGACCTGCTGGAGAACCT	720
Db	675	AACCATTTGGGACCCACCCCTAGCTCCAGTGCCCGGTTGAAAGATGATCTCTTTGAAAATTT	734
Qy	721	GCAGGCGCTACCAAGAGCGCATGGCGGTGCAGATGCAGCGCTTCAAGTGAAC	771
Db	735	GCAGGCGCTACCAAGAACCGATGGGAGTGCAAAATGACGCATTCAGAGTGATC	785

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RESULT 11
US-10-734-373-1
; Sequence 1, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EO-1-C2-1
; CURRENT APPLICATION NUMBER: US/10734,373
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
; US-10-734-373-1

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Query Match	62.9%	Score 487.4	DB 7	Length 1023
Best Local Similarity	76.9%	Pred. No. 2.2e-106		
Matches 593	Conservative 1	Mismatches 177	Indels 0	Gaps 0
Qy	1	AGATCTAAAGATGACCTGCTCCGAGGTGGAGACCTACGTCGTGAGCATCATCCCCAG	60	
Db	15	ATATTTAAAGATGAGTCTTCTGACCGAGGTGGAAACGTACGTTCTCTATCGTACCATC	74	
Qy	61	CGGCCCCCTGAAGCGCCGAGATCGCCACAGAGGCTCGAGGACGTGTTCCGCGGCAAGAACAC	120	
Db	75	AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGCTTTTGCAGGGAAGAACAC	134	
Qy	121	CGACCTGGAGGTGCTGATGGAGTGGCTGTAAGACACAGGCCCATCTGAGCGCCCTGACCAA	180	
Db	135	CGATCTTTGAGGCACTCATGGAAATGGCTAAAGACAAGACCAATCTCTGTCACTCTGACTAA	194	
Qy	181	GGGGATCCTGGGCTTCGTGTTCCCTGACCGTCGCCAGCAGCGCGCCTGACGCGCG	240	
Db	195	AGGGATTTTAGGATTCGTATTTCACGCTCACCGTGCCTCAGTAGCGAGAGACTGCAGGTAG	254	
Qy	241	CCGCTTCGTGCAGAACGCCCTTGAAACGGCAACGGGCAACCCCAACAAATGGACAAGGCCGT	300	
Db	255	ACGCTTTGTCCAAATAATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCACT	314	
Qy	301	GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAGGAGATCAGCCT	360	
Db	315	AAAACTGTACAGGAAGCTTAAAGAGAGAAATAACATTCATTCCATGGGGCAAAAGAGTGGCACT	374	

; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18593
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; US-10-434-811A-4

Query Match 62.5%; Score 484.6; DB 7; Length 1023;
Best Local Similarity 76.8%; Pred. No. 1e-105;
Matches 592; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

Qy 1 AGATCTAAAGATGAGCCCTGTGACCGAGGTGGAGACCTACGTGCTGAGCAGCATATCCCCAG 60
Db 15 ATATTTAAAGATGAGTCTCTGACCGAGGTGCAACGCTACGTCTCTCTATCTTACCATC 74

Qy 61 CGGCCCTCTGAAGCCGAGATCGCCGAGAGCTGGAGACGTGTTCCGCCGCAAGAACAC 120
Db 75 AGGCCCTCTCAAGCCGAGATCGCGCAGAGACTTTGAAGATGTCTTTGCAGGGGAAGAAC 134

Qy 121 CGACCTGGAGGTGCTGATGGAGTGGCTGAAGACGAGGCCATCTCTGAGCCCCCTGACCAA 180
Db 135 CGATCTTGAGGACTCATGGAAATGGCTTAAGACAGACCAATCTGTCACTCTGACTAA 194

Qy 181 GGGCATCTGGGCTTCGTGTTTCACTGACCGTGCACGAGCGCGCCCTGCGAGCGCG 240
Db 195 AGGGATTTAGGATTCGTATTACGCTCACCGTCCCGAGTGAGCGAGGACTGCAGCGTAG 254

Qy 241 CGCTTCGTGAGAACGCCCTGAAGGCAACGGGACCCCAACACATGGACAGGCGGT 300
Db 255 ACGCTTTGTCCAAATGCCCTTAGTGGAAACGGAGATCCAAACCAACATGGACAGAGCAGT 314

Qy 301 GAAGCTGTACAGGAAGCTGAAGAGGAGATCACCTTCCACGCGCCCAAGGAGATCAGCCT 360
Db 315 AAAACTGTACAGGAAGCTTAAAGAGAAATTAACATTCATGGGGCAAAAGAGGTGGCACT 374

Qy 361 GAGCTACAGCGCGCGCCCTGGCCAGCTGCATGGCCCTGATCTACAAACAGGATGGGCGC 420
Db 375 CAGCTATTCCACTGGTGCACTAGCCAGCTGCATGGGACTCATATACACAGAAATGGGAAC 434

Qy 421 CGTGACACCGAGGTGGCTTCGGCTGTGTGGCCACCTCGCAGGAGATCGCCGACAG 480
Db 435 TGTGACAAACGAAGTGGATTTGGCTGTGTATGGCCACATGTGAACAGATCGCTGATTC 494

Qy 481 CCAGCACCGCAGCAGCAGATGGTGACACCAACCAACCCCTGATCAGGCACGAGAA 540
Db 495 CCAGCATCGATCTCAGGCGAGATGGTGACAAATTAACCAACCAATTAATCAGACATGAANA 554

Qy 541 CAGGATGGTGTGGCCAGCACCAACCGCAAGGCCATGGAGCAGATGGCCGGCAGCAGCGA 600
Db 555 CAGAATGGTATTAGCCAGTACCACGGCTAAAGCCATGAAGCAGATGGCAGGGTCCAGTGA 614

Qy 601 GCAGGCCCGCAGGCGCATGGAGGTGGCCAGCCAGGCGAGATGGTGCAGGCCATGAG 660
Db 615 GCAGGCAGCAGAGGCGCATGGAGGTGGCTAGTAAGGCTAGGCGAGATGGTACAGGCAATGAG 674

Qy 661 GACCATCGGCCCAACCCAGCAGCGCGGCTGAAGAACGACCTGTGGGAGAACCT 720
Db 675 AACCATTTGGGACCCACCCCTAGCTCCAGTGCCTGGTTTGAAGATGATCTCTCTTGAANAATTT 734

Qy 721 GCAGGCTTACCAGAGCGCATGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
Db 735 GCAGGCTTACCAGAGCGCATGGCGTGCAGATGCAGCGCTTCAAGTGAAC 785

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GenCore version 5.1.7
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Run on: March 20, 2006, 23:50:55 ; Search time 352.218 Seconds
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Searched: 8023312 seqs, 1165852854 residues
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Listing first 45 summaries

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9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB_seq.*
10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB_seq2.*
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12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB_seq4.*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB_seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	733.6	94.7	756	12	US-11-131-479-27
2	692.8	89.4	1050	12	US-11-131-479-59
3	688.6	88.9	759	12	US-11-131-479-69
4	668.2	86.2	982	12	US-11-131-479-61
5	667.8	86.2	759	12	US-11-131-479-79
6	597.6	77.1	756	12	US-11-131-479-26
7	491.6	63.4	756	12	US-11-131-479-3
8	484.6	62.5	1027	12	US-11-131-479-3
9	476.6	61.4	1305	12	US-11-131-479-45
10	463.4	59.8	987	12	US-11-155-478A-131
11	457	59.0	982	12	US-11-131-479-60
12	457	59.0	4822	12	US-11-131-479-95
13	457	59.0	5161	12	US-11-131-479-101
14	457	59.0	5398	12	US-11-131-479-91
15	457	59.0	7798	12	US-11-131-479-97
16	457	59.0	7798	12	US-11-131-479-98
17	457	59.0	7798	12	US-11-131-479-99
18	457	59.0	7798	12	US-11-131-479-100
19	457	59.0	8442	12	US-11-131-479-106
20	457	59.0	8442	12	US-11-131-479-107

21	457	59.0	8450	12	US-11-131-479-104	Sequence 104, App
22	457	59.0	8450	12	US-11-131-479-105	Sequence 105, App
23	455.8	58.8	1027	12	US-11-155-478A-130	Sequence 130, App
24	401.8	51.8	629	9	US-11-137-807-18	Sequence 18, Appl
25	70.8	9.1	1521	12	US-11-129-442-22	Sequence 22, Appl
26	68.4	8.8	1566	12	US-11-131-479-33	Sequence 33, Appl
27	68.4	8.8	1566	12	US-11-131-479-35	Sequence 35, Appl
28	66.6	8.6	5278	12	US-11-124-602-2	Sequence 2, Appl1
29	66.6	8.6	5304	12	US-11-124-602-1	Sequence 1, Appl1
30	66.2	8.5	2430	7	US-10-649-457-3	Sequence 3, Appl1
31	65.2	8.4	1494	8	US-10-763-712A-173	Sequence 173, App
32	64.8	8.4	1092	12	US-11-014-842A-40	Sequence 40, Appl
33	63.4	8.2	1497	12	US-11-131-479-24	Sequence 24, Appl
34	62.8	8.1	1218	9	US-11-096-568A-12913	Sequence 12913, A
35	62.4	8.1	1432	12	US-11-000-688-1223	Sequence 1223, Ap
36	62.4	8.1	1683	12	US-11-131-479-37	Sequence 37, Appl
37	62	8.0	1913	9	US-11-096-568A-23950	Sequence 23950, A
38	61.6	7.9	1815	9	US-11-096-568A-22463	Sequence 22463, A
39	60.6	7.8	678	9	US-11-187-622-11	Sequence 11, Appl
40	60.2	7.8	2250	12	US-11-052-554A-532	Sequence 532, App
41	60.2	7.8	2295	7	US-10-649-457-1	Sequence 1, Appli
42	60	7.7	3624	7	US-10-755-092-6	Sequence 6, Appli
43	59.8	7.7	1325	9	US-11-096-568A-1077	Sequence 1077, Ap
44	59.4	7.7	864	12	US-11-179-411-26	Sequence 26, Appl
45	59.4	7.7	864	12	US-11-175-766-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-11-131-479-27
; Sequence 27, Application US/111311479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein
US-11-131-479-27

Query Match	94.7%	Score	733.6	DB	12	Length	756
Best Local Similarity	98.1%	Pred. No.	1.4e-149				
Matches	742	Conservative	0	Mismatches	14	Indels	0
Gaps	0						
Qy	11	ATGAGCTGCTGACCGAGGTGGAGACCTAGCTGCTGAGCATCATCCCGCGGCGGCCCCCTG	70				
Db	1	ATGAGCTGCTGACCGAGGTGGAGACCTAGCTGCTGAGCATCATCCCGCGGCGGCCCCCTG	60				
Qy	71	AAGCGCCGAGATGCCCGAGGCTGGAGGAGCTGTTCGCGGCGAAGAACACCGACCTGGAG	130				
Db	61	AAGCGCGAGATGCCCGAGGCTGGAGGAGCTGTTCGCGGCGAAGAACACCGACCTGGAG	120				
Qy	131	GTGCTGATGAGTGGCTGAAGACACGAGCCCATCTGTAGGCCCTTGACCAAGGGCATCTG	190				
Db	121	GTGCTGATGAGTGGCTGAAGACACGAGCCCATCTGTAGGCCCTTGACCAAGGGCATCTG	180				

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QY 191 GGCTTCGTGTTACCTGACCGTGCACCGAGCGCGCTGCGAGCGCGCGCTTCGTG 250
Db 181 GGCTTCGTGTTACCTGACCGTGCACCGAGAGGGGCTGCGAGAGGAGGTTCCGTG 240
QY 251 CAGAAACCCCTGAAACGGCGACCGGACCGCCCAACAACTGGAACAGGCGCTGAAAGCTGTAC 310
Db 241 CAGAAACCCCTGAAACGGCGACCGGCGACCCCAACAACTGGAACAGGCGCTGAAAGCTGTAC 300
QY 311 AGGAAGCTGAAGAGGGAGATCACCTTCCAGCGGCCCAAGGAGATCAAGCTGAGCTACAGC 370
Db 301 AGGAAGCTGAAGAGGGAGATCACCTTCCAGCGGCCCAAGGAGATCAAGCTGAGCTACAGC 360
QY 371 GCCGGCGCCCTGGCCAGCTGACCTGGGCTGTATCTACAACAGGATGGGGCGCGTGAACACC 430
Db 361 GCCGGCGCCCTGGCCAGCTGACCTGGGCTGTATCTACAACAGGATGGGGCGCGTGAACACC 420
QY 431 GAGGTGGCTTTCGGCCCTGGTGGCGCACCTGCGAGCAGATCGCGCGAGCAGCAGCCGC 490
Db 421 GAGGTGGCTTTCGGCCCTGGTGGCGCACCTGCGAGCAGATCGCGCGAGCAGCAGCCGC 480
QY 491 AGCCACAGGCGAGATGGTGACCAACCAACCCCTGTATCAGGCAACGAGAAACAGGATGGT 550
Db 481 AGCCACAGGCGAGATGGTGACCAACCAACCCCTGTATCAGGCAACGAGAAACAGGATGGT 540
QY 551 CTGCGCAGCACCACCGCCAGGCCATGGAGCAGATGGCGCGCAGCAGGAGCGCGCC 610
Db 541 CTGCGCAGCACCACCGCCAGGCCATGGAGCAGATGGCGCGCAGCAGGAGCGCGCC 600
QY 611 GAGGCCATGAGAGTGGCGCAGCGCAGGCGAGGATGGTGAGGCGCATGAGGACCATCGGC 670
Db 601 GAGGCCATGAGAGTGGCGCAGCGCAGGCGAGGATGGTGAGGCGCATGAGGACCATCGGC 660
QY 671 ACCCAACCCAGCAGCAGCGCGCTGGAAGAACGACCTGTGTGGAGAACCTGCGAGGCGCTAC 730
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QY 731 CAGAAGCGCATGGCGGTGCAGATGAGCGCTTCAAG 766
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RESULT 2

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US-11-131-479-59
; Sequence 59, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 59
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Open Reading Frame for the M2M1 Fusion from VR4755
US-11-131-479-59
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Query Match 89.4%; Score 692.8; DB 12; Length 1050;
Best Local Similarity 93.9%; Pred. No. 9.1e-141;
Matches 721; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 2 GATCTAAGATGAGCCTGCTGACCGAGGTGGAGACCTAGCTGCTGAGCATATCCCCAGC 61
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Db 283 GAGCTGGAGATGTCCTGCTGACAGAGTGGAACATACGTGCTGAGCATCGTCCGACG 342
QY 62 GGCCCCCTGAAGCCCGAGATCGCCAGAGGCTGGAGACGTGTTCCGCGGCAAGAACACC 121
Db 343 GGCCCCCTGAAGCCCGAGATCGCCAGAGACTGGAGACGTGTTCCGCGGCAAGAACACC 402
QY 122 GACTTGGAGTGTGATGGTGGCTGAAGACAGAGCCCATCTGTAGCCGCCCTGACCAAG 181
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QY 182 GGCATCTCGGCTTCGTGTTACCTGACCGTGCACGAGCGCGCTGTCAGCGCGCC 241
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QY 242 CGCTTTCGTGAGAACCGCTGAAACGGCAACCGCGACCCCAACATGGAAGAGCGCGTG 301
Db 523 AGATTTCGTGAGAACCGCTGAAACGGCAACCGCGACCCCAACATGGAAGAGCGCGTG 582
QY 302 AGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCAGCGGCCCAAGGAGATCAGCCTG 361
Db 583 AGCTGTACCGGAAGCTGAAGAGAGAGATCACCTTCCAGCGGCCCAAGGAGATCAGCCTG 642
QY 362 AGCTACAGCGCCCGCGCTTGGCCAGCTGCATGGGCTGTATCTACAACAGATGGGCGCC 421
Db 643 AGCTACAGCGCCCGCGCTTGGCCAGCTGCATGGGCTGTATCTACAACAGATGGGCGCC 702
QY 422 GTACCAACCAAGAGTGCCCTTCGCGCTGGTGGCGCACCTGCGAGCAGATGCGCGCAGC 481
Db 703 GTGACCACCAAGAGTGGCTTTCGCGCTGGTGGCGCACCTGCGAGCAGATGCGCGCAGC 762
QY 482 CAGCACCGCAGCACACAGGAGATGGTGACCAACCAACCAACCCCTGTATCAGGCAAGAAC 541
Db 763 CAGCACAGAAAGCACACAGAGATGGTGGCGCACCAACCAACCCCTGTATCAGACAGAAC 822
QY 542 AGGATGCTGTGCTGCGCAGCACACCGCCAGGCCATGGAGCAGATGGCGCGCAGCAGCGAG 601
Db 823 AGAATGCTGTGCTGCGCAGCACACCGCCAGGCCATGGAGCAGATGGCGCGCAGCAGCGAG 882
QY 602 CAGCGCCCGCAGAGCCATGGAGTGGCGCAGCCAGGCCAGGAGATGTTGTCAGGCGCATGAGG 661
Db 883 CAGCGCCCGCAGAGCCATGGAGATCGCCAGCGCAGGCGCAGACAGATGTTGTCAGGCGCATGAGA 942
QY 662 ACATCGGCGACCCACCCAGCAGCAGCGCGCGCTGGAAGACCGACCTGTGGAGAACCTG 721
Db 943 GCCATCGGCGACCCACCCAGCAGCAGCGCGCGCTGGAAGACCGACCTGTGGAGAACCTG 1002
QY 722 CAGGCGCTTACCAGAAAGCGCATGGCGGTGCAGATGCGCGCTTCAAGTGA 769
Db 1003 CAGACCTTACCAGAAAGAGATGGCGGTGCAGATGCGAGAGATTCAGTGA 1050
```

RESULT 3

```
US-11-131-479-69
; Sequence 69, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 69
; LENGTH: 759
```

```
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Open Reading Frame for M1 Gene from VR4760
US-11-131-479-69

Query Match      88.9%; Score 688.6; DB 12; Length 759;
Best Local Similarity 94.2%; Pred. No. 7.5e-140;
Matches 715; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 11 ATGAGCTGCTGACCGAGGTGGAGACCTACGTGTGAGCATATCCCGAGGGCCCCCTG 70
Db 1 ATGCTCCCTGCTGACAGAGTGGAAACATACGTGTGAGCATGCGCCAGCGGCCCTG 60

Qy 71 AAGGCCGAGATCGCCGAGGCTGGAGAGCTGTTGGCCGGAAGAACACCGACCTGGAG 130
Db 61 AAGGCCGAGATCGCCGAGGCTGGAGAGCTGTTGGCCGGAAGAACACCGACCTGGAG 120

Qy 131 GTGCTGATGGAGTGGCTGAAGACAGGCGCCATCTCTGAGCCCTTGACCAAGGGCATCTG 190
Db 121 GCCCTGATGGAGTGGCTGAAGACAGGCGCCATCTCTGAGCCCTTGACCAAGGGCATCTG 180

Qy 191 GGCTTCGTGTTACCTGACCGTGCAGCGAGCGCGCTGCGAGCGCGCGCTTCTGTG 250
Db 181 GGCTTCGTGTTACCTGACCGTGCAGCGAGCGCGCTGCGAGCGCGCGCTTCTGTG 240

Qy 251 CAGAACGCCCTGAACGGCAACGGGACCCCAACCAACATGGACAAGGCCGTGAAGCTGTAC 310
Db 241 CAGAACGCCCTGAACGGCAACGGGACCCCAACCAACATGGACAAGGCCGTGAAGCTGTAC 300

Qy 311 AGGAAGCTGAAGAGGGAGATCACCTTCCACGGCCCAAGGAGATCAGCTTGAGCTACAGC 370
Db 301 CGGAAGCTGAAGAGAGATCACCTTCCACGGCCCAAGGAGATCAGCTTGAGCTACAGC 360

Qy 371 GCCGGCGCTGGCGAGCTGATGGGCTGTATCTAACAAGAGTGGGCGCGCTGACCAACC 430
Db 361 GCCGGCGCTGGCGAGCTGATGGGCTGTATCTAACAAGATGGGCGCGCTGACCAACC 420

Qy 431 GAGGTGGCTTGGCGCTGGTGGCGCACCTGCGAGCAGATCGCGGACAGCCAGCACCGC 490
Db 421 GAGGTGGCTTGGCGCTGGTGGCGCACCTGCGAGCAGATCGCGGACAGCCAGCACCGC 480

Qy 491 AGCCACAGCAGATGGTGACCAACCAACCCCTGTATCAGGCAAGAGAAAGAGATGGTG 550
Db 481 AGCCACAGCAGATGGTGACCAACCAACCCCTGTATCAGACAGAGAACAGATGGTG 540

Qy 551 CTGGCCAGCAACACCGCAAGGCCATGGAGCAGATGGCCGCGCAGCAGCGAGCGCGCC 610
Db 541 CTGGCCAGCAACACCGCAAGGCCATGGAGCAGATGGCCGCGCAGCAGCGAGCGCGCC 600

Qy 611 GAGGCCATGAGGTGGCGAGCGCAGGCGCAGATGGTGAGGCGCATGAGGACCATCGGC 670
Db 601 GAGGCCATGAGGTGGCGAGCGCAGGCGCAGATGGTGAGGCGCATGAGGACCATCGGC 660

Qy 671 ACCCACCCAGCAGCGCGCGCTGAAGAAACGACCTGTGAGAGAACCTTCAGGCGCTTAC 730
Db 661 ACCCACCCAGCAGCGCGCGCTGAAGAAACGACCTGTGAGAGAACCTTCAGGACCTTAC 720

Qy 731 CAGAAGCGCATGGGCGTGCAGATGACGCGCTTCAAGTGA 769
Db 721 CAGAAGAGAAATGGGCGTGCAGATGACAGATTTCAAGTGA 759
```

RESULT 4

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US-11-131-479-61
; Sequence 61, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
```

```
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 982
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Codon Optimized Segment 7 from VR4763
US-11-131-479-61
```

```
Query Match      86.2%; Score 668.2; DB 12; Length 982;
Best Local Similarity 92.4%; Pred. No. 1.9e-135;
Matches 703; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 11 ATGAGCTGCTGACCGAGGTGGAGACCTACGTGTGAGCATATCCCGAGGGCCCCCTG 70
Db 1 ATGAGCTGCTGACCGAGGTGGAAACGTATGTTCTCTATCGTGCAGCGGCCCTG 60

Qy 71 AAGGCCGAGATCGCCGAGGCTGGAGAGCTGTTCCCGGCAAGAACACCGACCTGGAG 130
Db 61 AAGGCCGAGATCGCCGAGGCTGGAGAGCTGTTCCCGGCAAGAACACCGACCTGGAG 120

Qy 131 GTGCTGATGGAGTGGCTGAAGACAGGCGCCATCTCTGAGCCCTTGACCAAGGGCATCTG 190
Db 121 GCCCTGATGGAGTGGCTGAAGACAGGACCCATCTCTGAGCCCTTGACCAAGGGCATCTG 180

Qy 191 GGCTTCGTGTTACCTGACCGTGCAGCGAGCGCGCTGCGAGCGCGCGCTTCTGTG 250
Db 181 GGCTTCGTGTTACCTGACCGTGCAGCGAGAGGCGCTGCGAGAGAAAGATTCGTG 240

Qy 251 CAGAACGCCCTGAACGGCAACGGGACCCCAACCAACATGGACAAGGCCGTGAAGCTGTAC 310
Db 241 CAGAACGCCCTGAACGGCAACGGGACCCCAACCAACATGGACAAGGCCGTGAAGCTGTAC 300

Qy 311 AGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCAAAGAGATCAGCTTGAGCTACAGC 370
Db 301 AGAAGCTGAAGAGAGAGATCACCTTCCACGGCGCCAAAGAGATCGCCCTGAGCTACAGC 360

Qy 371 GCCGGCGCTGGCGAGCTGATGGGCTGTATCTAACAAGAGTGGGCGCGCTGACCAACC 430
Db 361 GCCGGCGCTGGCGAGCTGATGGGCTGTATCTAACAAGAAATGGGCGCGCTGACCAACC 420

Qy 431 GAGGTGGCTTGGCGCTGGTGGCGCACCTGCGAGCAGATCGCCGACAGCCAGCACCGC 490
Db 421 GAGGTGGCTTGGCGCTGGTGGCGCACCTGCGAGCAGATCGCCGACAGCCAGCACAGA 480

Qy 491 AGCCACAGGAGATGGTGACCAACCAACCCCTGTATCAGGCAAGAGAAAGAGATGGTG 550
Db 481 AGCCACAGAGATGGTGACCAACCAACCCCTGTATCAGACAGAGAACAGATGGTG 540

Qy 551 CTGGCCAGCAACACCGCAAGGCCATGGAGCAGATGGCCGCGCAGCAGCGAGCGCGCC 610
Db 541 CTGGCCAGCAACACCGCAAGGCCATGGAGCAGATGGCCGCGCAGCAGCGAGCGCGCC 600

Qy 611 GAGGCCATGAGGTGGCGAGCGCAGGCGCAGATGGTGAGGCGCATGAGGACCATCGGC 670
Db 601 GAGGCCATGAGGTGGCGAGCGCAGGCGCAGATGGTGAGGCGCATGAGGACCATCGGC 660

Qy 671 ACCCACCCAGCAGCGCGCGCTGAAGAAACGACCTGTGAGAGAACCTTCAGGCGCTTAC 730
Db 661 ACCCACCCAGCAGCGCGCGCTGAAGAAAGATGATCTTCTTGAATAATTTGACAGCTTAT 720

Qy 731 CAGAAGCGCATGGGCGTGCAGATGACGCGCTTCAAGTGAAC 771
Db 721 CAGAAACGAATGGGCGTGCAGATGACACGATTCAAGTGACC 761
```

RESULT 5
 US-11-131-479-79
 ; Sequence 79, Application US/11131479
 ; Publication No. US20060024670A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Luke, Catherine J.
 ; APPLICANT: Vilalta, Adrian
 ; APPLICANT: Wloch, Mary K.
 ; APPLICANT: Evans, Thomas G.
 ; APPLICANT: Geall, Andrew J.
 ; APPLICANT: Jimenez, Gretchen
 ; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
 ; FILE REFERENCE: 1530.0640002/EJH/J-H
 ; CURRENT APPLICATION NUMBER: US/11/131,479
 ; CURRENT FILING DATE: 2005-05-18
 ; PRIOR APPLICATION NUMBER: US 60/571,854
 ; PRIOR FILING DATE: 2004-05-18
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 79
 ; LENGTH: 759
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Optimized M1 Coding Region
 ; US-11-131-479-79

 Query Match 86.2%; Score 667.8; DB 12; Length 759;
 Best Local Similarity 92.5%; Pred. No. 2.3e-135;
 Matches 702; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

 QY 11 ATGAGCCTGTCGACCGAGGTGGAGACTTACGTCTGAGCATCATCCCGAGCGCCCCCTG 70
 DB 1 ATGAGCCTGTCGACCGAGGTGGAGACTTCTCTATCGTGCCTGAGCGCGCCCCCTG 60

 QY 71 AAGCGCGAGATCCCGAGAGCTGGAGAGCTGTTCGCGGCAAGAACACCGACCTGGAG 130
 DB 61 AAGCGCGAGATCCCGAGAGCTGGAGAGCTGTTCGCGGCAAGAACACCGACCTGGAG 120

 QY 131 GTGCTGATGAGTGGCTGAAGACAGCGCCCATCTTGAGCCCCCTGACCAAGGCGCATCTG 190
 DB 121 GCCTGATGAGTGGCTGAAGACAGACCCATCTTGAGCCCCCTGACCAAGGCGCATCTG 180

 QY 191 GGCTTCGTGTACCTGACCTGCCAGCGAGCGCGCTGACGCGCGCCGCTTCGTG 250
 DB 181 GGCTTCGTGTACCTGACCTGCCAGCGAGAGGCTGTCAGAGAGAAAGATTCTGTG 240

 QY 251 CAGAACCCCTGTAACGCGCAACGCGACCCCAACATGAGCAAGCCGTGAAGCTGTAC 310
 DB 241 CAGAACCCCTGTAACGCGCAACGCGACCCCAACATGAGCAAGCCGTGAAGCTGTAC 300

 QY 311 AGGAAGCTGAAGGGAGATCACCTTCCACGGCGCCAGAGAGATCAGCCTGAGCTACAGC 370
 DB 301 AGGAAGCTGAAGGGAGATCACCTTCCACGGCGCCAGAGAGATCAGCCTGAGCTACAGC 360

 QY 371 GCGGCGCCCTGGCAGCTCATGGGCTGATCTACACAGAGATGGCGCGCTGACAC 430
 DB 361 GCGGCGCCCTGGCAGCTCATGGGCTGATCTACACAGAGATGGCGCGCTGACAC 420

 QY 431 GAGGTGCTTGGGCTGTGTGGCCACCTGGGAGCAGATCGCCGACAGCAGCACCGC 490
 DB 421 GAGGTGCTTGGGCTGTGTGGCCACCTGGGAGCAGATCGCCGACAGCAGCACAG 480

 QY 491 AGCCACAGGAGATGTGTGACCAACCAACCCCTGATCAGGACGAGAACAGGATGGTG 550
 DB 481 AGCCACAGGAGATGTGTGACCAACCAACCCCTGATCAGGACGAGAACAGGATGGTG 540

 QY 551 CTGGCAGACACCGCCAGGCGCATGGAGCAGATGGCGGCGAGCGAGCGCGCGCC 610
 DB 541 CTGGCAGACACCGCCAGGCGCATGGAGCAGATGGCGGCGAGCGAGCGCGCGCC 600

 QY 611 GAGGCCATGAGGTGGCGACGACGAGCGCAGGACAGATGTGTGAGGCCATGAGGACCATCGGC 670

Db 421 GAGGTAGCCTTTGGCCTGCTGGCCACATTGGCAGCAGATCGCGCATCTCAGCATAGA 480
QY 491 AGCCACAGCAGATGGTGACACACCAACACCCCTGATCAGGCACGAGAACAGGATGGT 550
Db 481 TCTCAGACAGATGGTGACGACTATCAAAACCCCTGATACGGCAGCAGAACAGGATGGT 540
QY 551 CTGGCCAGCACACCGCCCAAGGCCATGAGAGCAGATGGCCGGCAGCAGCAGCGCCGCC 610
Db 541 CTGGCCTCTACTACCGCCCAAGGCCATGAGCAGATGGCCGGCAGCAGTGGAGCGCCGCC 600
QY 611 GAGGCCATGAGAGTGGCCAGCAGCAGCCAGGACGATGGTGAGGCCATGAGGACCATCGGC 670
Db 601 GAGGCCATGAGAGTGGTTCACAGGCCAGGAGATGGTGAGGCCATGCGGAACCATCGGC 660
QY 671 ACCACCCAGCAGCAGCGCGGCCCTGAAGACGACCTGCTGGAGAACCTCAGGSCCTAC 730
Db 661 ACTCACCCCTCAGCTCTGGCGGCTTGAAGAACGACCTGCTGGAGAACCTCAGGSCCTAT 720
QY 731 CAGAAGCGCATGGCGGTGCAGATGACGCGCTTCAAG 766
Db 721 CAGAAGAGATGGCGGTACAGATGCAGAGGTTCAAG 756

RESULT 7

US-11-131-479-26
; Sequence 26, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein
US-11-131-479-26

Query Match 63.4%; Score 491; DB 12; Length 756;
Best Local Similarity 78.1%; Pred. No. 3.4e-97;
Matches 590; Conservative 0; Mismatches 165; Indels 0; Gaps 0;
QY 11 ATGAGCCTGCTGACCGAGTGGAGACCTGCTGCTGAGCATATCCCGAGCGCCCTG 70
Db 1 ATGAGCTTGCTAACAGAGTGGAAACCTATGCTCTCAGTATCATCTCTAGCGGCCCTTA 60
QY 71 AAGGCCAGATGCCCCAGAGCTGGAGGACGTGTTCGCCGCAAGAACACCGACTGGAG 130
Db 61 AAAGCCGAATCGCTCAGCGCTCGAGGATGTTTTTGGCGCAAGAAACACCGACTGGAG 120
QY 131 GTGCTGATGGATGGCTGAAGACCAAGGCCCATCTCTGAGCCCTCCCTGACCAAGGGCATCTG 190
Db 121 GTATTGATGGATGGCTGAAACCGGACCTTATCTGAGCCCTCCCTGACTAAGGGAATCTC 180
QY 191 GCCTTCGTGTTTACCTCAGCGTCCAGCGAGCGCGCTTGCAGCGCGCGCTTCTG 250
Db 181 GCCTTCGTGTTTACCTCAGCGTCCCTCAGAGGGGTCTTCAAAGAGGCGCTTCTG 240
QY 251 CAGAACCGCTTGAACCGGCAACCGGACCCCAACACATGGAACAAGGCGGTGAAGCTGTAC 310
Db 241 CAGAAGCGCTTAAACCGGGAACCGGGAACCGGACCCAAATATATGATAGGCGAGTGAACCTGTAT 300

QY 311 AGGAAGCTGAAGAGGGAGATCACCTTCCACGGGCCCAAGAGATCAGCCTGAGCTACAGC 370
Db 301 CGCAATTAAGCGGGAGATAACCTTCCATGGAGCCAAAGAGATCTCCCTGTCTTACTCT 360
QY 371 GCGCGCCCTTGGCCAGCTGCATGGGCTGATCTTACCAAGGATGGCGCGCGTGAACACC 430
Db 361 GCAGGTGCTCTCGCGTCTGTATGGGACTTATCTTAAACCGAATGGCGCGCTCAACA 420
QY 431 GAGGTGGCCTTCGCGCTGCTGGCCACCTGCGAGCAGATCGCGGACGACGACGACCGC 490
Db 421 GAAGTGGCTTTCGCGGCTGGTGGCGAACTTGGCAACAGATTGCTGACAGTCAAGACCGG 480
QY 491 AGCCACAGGACAGATGGTGACCAACCAACCCCTGATCAGGCACGAGAACAGGATGGT 550
Db 481 TCCACCGCTCAATGGTGACCAACCAACCAATCCGCTGATGACATGAATCGCATGGTT 540
QY 551 CTGGCCAGCACACCGCCCAAGGCCATGAGAGCAGATGGCCGGCAGCAGCAGCGCCGCC 610
Db 541 CTAGCATCAACTACAGCCAAAGCAATGGAAACAAATGGCCGGAAGCTCCGAGCAGGCTGCC 600
QY 611 GAGGCCATGAGAGTGGCCAGCAGCGCCAGGACGAGATGGTGAGGCCATGAGGACCATCGGC 670
Db 601 GAGCGATGAGAGTGGCGTCTCCAGGCCAGACAGATGGTGATAGGAACTATCGGT 660
QY 671 ACCCACCCAGCAGCAGCGCGCTTCAAGAACGACCTGCTGGAGAACCTTCCAGGCTTAC 730
Db 661 ACGACCCAAAGTCTTTCAGCTGGGCTGAAGATGATCTTCTTGAGAACCTTCCAGGCTTAC 720
QY 731 CAGAAGCGCATGGCGGTGCAGATGACGCGCTTCA 765
Db 721 CAAAGCGGATGGCGCTCCAGATGCAGAGATTTAA 755

RESULT 8

US-11-131-479-3
; Sequence 3, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Influenza A virus
US-11-131-479-3

Query Match 62.5%; Score 484.6; DB 12; Length 1027;
Best Local Similarity 76.8%; Pred. No. 8e-96;
Matches 592; Conservative 0; Mismatches 179; Indels 0; Gaps 0;
QY 1 AGATCTAAAGATGAGCTGCTGACCGAGGTGGAGACCTAGTGTGATGAGCATCATCCCCAG 60
Db 16 ATATTGAAGATGAGTCTTCTAACCGAGGTGCAAAACGTAGCTACTCTCTATCATCCCCGC 75
QY 61 CGGCCCCCTCAAGCCGAGATCGCCAGAGCTGGAGAGCTGTTCGCCCGCAAGAACAC 120
Db 76 AGGCCCCCTCAAGCCGAGATCGCACAGACTTTGAAGATGTCTTTGAGGGAAGAACAC 135
QY 121 CGACTTGAGGTGCTGATGGAGTGGCTGGAAGACGAGGCCCATCTCTGAGCCCCCTGACCAA 180

Db 136 TGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCTGTCACTCTGACTAA 195
Qy 181 GGGCATCCTGGGCTTCGTGTTCACTCCCTGACCGTCCAGCGAGCGCGCTTGACGCCG 240
Db 196 GGGGATTTAGGATTTGTGTTTCACGCTCACCGTCCCGCAGTGAGCGAGCTGCAGCGTAG 255
Qy 241 CCGCTTCGTGAGAACCGCCCTGAACGGCAACGGCGACCCCAACAACATGACAGCGCGT 300
Db 256 ACGCTTTTCCAAATGCCCTTAATGGGAACGGGGATCCAAATAACTGATGACAAAGCAGT 315
Qy 301 GAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCCCAAGGAGATCACGCT 360
Db 316 TAAACTGTATAGGAAGCTCAAGAGGAGATNAATTCATGGGGCCAAAGAAATCTCACT 375
Qy 361 GAGCTACAGCGCCGCGCCCTTGGCCAGCTGCATGGGCTGTATCAACAAGGATGGCGC 420
Db 376 CAGTTATTCGTGTCGTCACCTTGCAGTTGTATGGGCTCATATACAAACAGGATGGGGC 435
Qy 421 CGTGACACCGAGTGGGCTTCGGCGCTGGTGTGGCCACCTGCGAGCAGATCGCGACAG 480
Db 436 TGTGACCACTGAAGTGGCATTTGGCCCTGGTATGTGCAACCTGTGAACAGATTTGCTGACT 495
Qy 481 CCAGCAGCGACGACAGGAGATGTTGACCAACCAACCCCTGTATCAGGCACGAGAA 540
Db 496 CCAGCATGGTCTCATAGGCCAAATGGTGACAAACCAATCCACTAATCAGACATGAGAA 555
Qy 541 CAGGATGGTGTGTCGACGACCAACCGCCAGCGCATGGAGCAGATGCCCGCAGCAGCGA 600
Db 556 CAGAAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGAGCAATGGCTGGATCGAGTGA 615
Qy 601 GCAGGCGCCGAGCGCATGAGGTGGCCAGCCAGCGCCAGCGCAGGATGGTGAGGCCATGAG 660
Db 616 GCAAGCAGCAGAGGCCATGGAGGTTGTCTAGTTCAGGCTAGACAAATGGTGCAAGCGATGAG 675
Qy 661 GACCATGGCACCCACCCAGCAGCGCGGCTGAAGAACGACCTGCTGGAGAACCT 720
Db 676 AACCATTTGGGACTCATCTAGCTCAGTGTCTGAAATGATCTTCTTGAATTT 735
Qy 721 GCAGGCTTACCAGAACGCGCATGGGCGTGCGATGCGCGCTTCAAGTGAAC 771
Db 736 GCAGGCTTATCAGAAACGAATGGGGTGCGAGATCAACGGTTCAAGTGATC 786

RESULT 9

US-11-131-479-45
; Sequence 45, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 1305
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Influenza A Virus M1 Fused to Synthetic HBcAg
US-11-131-479-45

Query Match 61.4%; Score 476; DB 12; Length 1305;
Best Local Similarity 76.9%; Pred No. 5, 7e-94;
Matches 581; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

Qy 11 ATGAGCCTGCTGACCGAGGTGGAGACCTAGCTGCTGAGCATCATCCCGAGCGCCCTTG 70
Db 1 ATGAGTCTTTCTAACCGAGGTGAAACGTACGTACTCTCTATCATCCCGTCAGGCCCCCTC 60
Qy 71 AAGGCCGAGATCCCGCAGAGGCTGGAGGAGCTGTTCGCGGCAAGAACACCCGACCTGGAG 130
Db 61 AAAGCCGAGATCCACAGAGACTTGAAGATGTCTTTGAGGGAAGAACACTGATCTTGAG 120
Qy 131 GTGCTGATGAGGTGGCTGAAGACAGGCCCATCTGAGCCCCCTGACCAAGGGGATCCTG 190
Db 121 GTTCTCATGAATGGCTAAAGACAAGACCAATCTGTCACTCTGACTAAGGGGATTTTA 180
Qy 191 GGGTTGTGTTTACCTGACCGTGCCAGGAGCGGGCTGACAGCGCCCGCTTCGTG 250
Db 181 GGATTTTGTGTTACGCTCACCGTGCCAGTGAGCGAGGACTGCAGCGTATGACGCTTTGTC 240
Qy 251 CAGAACGCCCTGAACGGCAACGGCGACCCCAACAATGGAACAAGGCCGTGAAGCTGTAC 310
Db 241 CAAATGCCCTTAATGGGAACGGGGATCCAAATTAACATGACAAAGCAGTTAACTGTAT 300
Qy 311 AGGAAGCTGAAGAGGAGATCACCTTCCAGCGGCCCAAGGAGATCAAGCTTGAGCTACAGC 370
Db 301 AGGAAGCTCAAGAGGAGATTAACATTCATGGGGCCAAAGAAATCTCACTCAGTTATTCT 360
Qy 371 GCCGGGCCCTGGCCAGCTGCTATGGGCTGATCTACAAAGGATGGGCGCCGTGACCCAC 430
Db 361 GCTGGTGCACTTGCCAGTTGTATGGGCTCATATACAAAGGATGGGGGCTGTGACCACT 420
Qy 431 GAGGTGCCCTTCGGCCCTGGTGTGGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGC 490
Db 421 GAAGTGGCATTTGGCCTGGTATGTGCAACTGTGAAACAGATTGCTGACTCCAGCATCGG 480
Qy 491 AGCCACAGGCGAGATGGTGACCAACCAACCCCTGATCAGGCAAGGAGATCAGATGGTG 550
Db 481 TCTCATAGGCAATGGTGACCAACCAATCCACTAATCAGACATGAGAAACAGAAATGGTT 540
Qy 551 CTGCCAGCACCAACCGCCAGGCCATGGAGCAGATGGCCGCGAGCAGCAGCGAGCGCCGC 610
Db 541 TTAGCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGGATCGAGTGAGCAAGCAGCA 600
Qy 611 GAGGCCATGAGGTGGCCAGCGCAGGCGAGGATGGTGCAGGCGCATGAGGACCATCGGC 670
Db 601 GAGGCCATGAGGTGCTAGTCTAGGCTAGACAAATGGTGCAGCGATGAGAACCATTTGGG 660
Qy 671 ACCCACCCAGCAGCAGCGCCGCTGAAAGAACGACTGCTGGAGAACCTTGCAGGCGCTAC 730
Db 661 ACTCATCTAGTCCAGTGTGGTCTGAAAAATGATCTTCTGAAAAATTTGACAGGCTAT 720
Qy 731 CAGNAGGCGATGGCGTGCGAGATGCGCGCTTCAAG 766
Db 721 CAGAAACGAATGGGGTGCGAGATGCAACGGTTCAAG 756

RESULT 10

US-11-155-478A-131
; Sequence 131, Application US/11155478A
; Publication No. US2006001410A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE LAVAL
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 174

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 987
; TYPE: DNA
; ORGANISM: human Influenza A virus
; FEATURE:
; NAME/KEY: Gene
; LOCATION: (1)...(987)
; OTHER INFORMATION: human Influenza A virus
; OTHER INFORMATION: strain A/Charlottesville/31/95 (H1N1)
; OTHER INFORMATION: accession number AF398876
US-11-155-478A-131

Query Match          59.8%; Score 463.4; DB 12; Length 987;
Best Local Similarity 75.6%; Pred. No. 3e-91;
Matches 575; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

Qy 11 ATGAGCTGTGACCGAGGTGGAGACCTACGTGTGAGCATATCCCGAGGCGCCCTG 70
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 ATGAGCTCTTAACCGAGGTGGAACGTACGTTCTCTATCGTCCCGTCAGGCGCCCTC 60
Qy 71 AAGCCGAGATCGCCAGAGCTGGAGACGTGTCGCCGCAAGAACACCGACTGGAG 130
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 AAGCCGAGATCGCCAGAGCTGGAAGATGCTTTGCTGGAAAGAACACCGACTTTGAG 120
Qy 131 GTGCTGTAGTGGAGTCAAGACAGGCGCCATCTGTGAGCCCTTGACCAAGGGATCCTG 190
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 GCTCTCATGGAGTGAAGACAGACCGATCTCTGTCACCTCTGACTAAGGGATTTTA 180
Qy 191 GGCTTGTGTTTCACTTGTGACCGAGCGCGCTGACGCGCGCGCTTGTG 250
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
181 GGATTTGTGTTTCACTTGTGACCGAGCGCGCTGACGCGCGCGCTTGTG 240
Qy 251 CAGAACGCTTGAAGGGAGATCACTTCCACGCGCGCAAGGAGATCAGCTGAGTACAGC 310
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
241 CAAATGCTCTTAATGGGAATGGGGATCCAAATTAACATGGACAGAGCTTTAAATCTGAT 300
Qy 311 AGGAAGCTGAAGGGAGATCACTTCCACGCGCGCAAGGAGATCAGCTGAGTACAGC 370
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 AGAAGCTTAAGGGAGATTAATTCATGGGGCAAGAAATAGCACTCAGTTATTCT 360
Qy 371 GCCGCGCTTGTGACCGAGCTGATGATTAACAAGGATGGCGCGCTGACCAACC 430
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
361 GCTGTGCACTTGTGACGTTGATGAGCAATGGCTGATGAGTGAACAGCAGCT 600
Qy 431 GAGGCGCTTGTGCGCGCTGATGCGCACCTGGAGCAGATCGCGCAGCAGCAGCGC 490
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
421 GAATCAGCATTTGGCTGATATGCGCAACCTGTGAACAGATTTGCTGACTCCAGCAGG 480
Qy 491 AGCCACAGGAGATGGTGACCAACCAACCCCTGTATCAGGCAAGAGATGAGATGGTG 550
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
481 TCTCATAGGCAATGGTGAACCAACCAATCCATTAATAGGCATGAGAACAGATGTT 540
Qy 551 CTGGCCAGCACACCGCAAGGCCATGGAGCAGATGGCGCGCAGCAGCAGCGCGCC 610
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
541 CTGGCCAGCACTACAGCTAAAGCTATGGAGCAATGGCTGATGAGTGAACAGCAGCT 600
Qy 611 GAGGCGATGAGGTGGCCAGGCGCAGGCAAGATGTTGAGGCGATGAGAACCATCGGC 670
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
601 GAGGCGATGAGGTGGCTAGTTCAGGCGAGGCAATGGTGCAGGCAATGAGAGCCATTGGG 660
Qy 671 ACCCAACCCAGCAGCGCGCTGAAGAACGACCTGTGGAGAACAGATGGTG 550
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
661 ACTCATCTAGCTTAGCACTGGCTTGAAGAACGACCTGTGGAGAACAGATGGTG 540
Qy 731 CAGAAGCGCATGGCGGTGCAGATGACGCGCTTCAAGTGAAC 771
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
721 CAGAAACGAATGGGGTGCAGATGCAACGATTTCAAGTGATC 761

RESULT 11
US-11-131-479-60
; Sequence 60, Application US/11131479
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Db 661 ACTCATCTAGCTCCAGTCTGGTCTAAAGATGATCTCTTGAATAATTGACAGACCTAT 720
Qy 731 CAGAAGCGCATGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
Db 721 CAGAAACGAATGGGGTGCAGATGCAACGATTCAAGTGACC 761

RESULT 12

US-11-131-479-95
; Sequence 95, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95
; LENGTH: 4822
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4764, Ligation of VR4756 RV-Sali into VR10682 RV
US-11-131-479-95

Query Match 59.0%; Score 457; DB 12; Length 4822;
Best Local Similarity 75.0%; Pred. No. 6.8e-90;
Matches 571; Conservative 0; Mismatches 190; Indels 0; Gaps 0;
Qy 11 ATGAGCCTGTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCTG 70
Db 814 ATGAGCCTTCTAACCGAGGTGCAACGATGTCTCTCTATCGTTCCATCAGGCCCTC 873
Qy 71 AAGCCGAGATCGCCAGAGCTGGAGGACGTGTTCGCCGCAAGAACACCGACTGGAG 130
Db 874 AAAGCCGAATCGCGCAGAGACTTGAAGATGTCTTTGCTGGGAAAAACACAGATCTTGAG 933
Qy 131 GTGCTGATGGAGTGGCTGAACAGCAGGCCCATCTCTGAGCCCTTGACCAAGGGCATCTG 190
Db 934 GCTCTCATGGAAATGGCTAAGACAGACCAATCTCTGACCTCTGACTAAGGGGATTTTG 993
Qy 191 GGCTTGTGTTTACCGTGCACCGTGCACGAGCGCGCTGCGAGCGCGCGCTTCGTG 250
Db 994 GGGTTGTGTTTACCGTGCACCGTGCACGAGGAGCTGCAGCGTAGCGCTTTGTC 1053
Qy 251 CAGAACGCCCTGAACGGCAACGGCGACCCCAACACATGGAACAGCCGCTGAAGCTGTAC 310
Db 1054 CAAAATGCCCTCAATGGGAATGGGGATCCAAATACATGAGCAGACGATTTAAACTATAT 1113
Qy 311 AGGAAGCTGAAGGGAGATCACCTTCCACGCGCCGAAGGAGATCAGCTCAGCTACAGC 370
Db 1114 AGAAAACCTTAAGAGGGAGATTACATTTCCATGGGGCCAAAGAAATAGCACTCAGTTATTCT 1173
Qy 371 GCCGCGCCCTTGGCAGCTGATGGGCTGTATCTACAAACAGATGGGCGCGTGAACCA 430
Db 1174 GCTGGTGACTTGGCAGTTGATGGGCTCATATACACAGATAGGGGCTGTAACTACT 1233
Qy 431 GAGTGGCTTTCGGCTGGTGGCCACCTGCGAGCAGATGCGCGACAGCCAGCGC 490
Db 1234 GAAGTGGCTTTCGGCTGGTATGTGCAACATGTGAACAGATTTGCTGACTCCCGACAGG 1293
Qy 491 AGCCACAGCGAGATGGTGACCAACCAACCCCTGATCAGGACGAGAACAGGATGGT 550

Db 1294 TCTCATAGGCATGTGGCAACCAACCAATCCATTAAATAGGCATGAGAACAGATGGTT 1353
Qy 551 CTGGCCAGCACCAACCGCAAGGCCATGAGCAGATGCGCGGAGCAGCAGCAGCGCCGCC 610
Db 1354 TTGGCCAGCACTACAGCTAAGGCTATGGAGCAAAATGGCTGGATCAAGTGAGCAGCG 1413
Qy 611 GAGGCCATGAGGTGGCCAGCGCAGCGCAGCAGATGCTGAGGACCATGAGCCATCGGC 670
Db 1414 GAGGCCATGGAATTTGCTAGTCAGGCGAGGCAATGCTGCGGCAATGAGGCCATTTGG 1473
Qy 671 ACCCAGCCAGCAGCAGCGCGCCCTGAAGAACGACCTGCTGGAGAACCTGCGAGGCTAC 730
Db 1474 ACTCATCTAGCTCCAGTGTGCTCTAAAAGATGATCTTCTTGAATAATTGACAGCTAT 1533
Qy 731 CAGAAGCGCATGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
Db 1534 CAGAAACGAATGGGGTGCAGATGCAACGATTCAAGTGACC 1574

RESULT 13

US-11-131-479-101
; Sequence 101, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 101
; LENGTH: 5161
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4770, M2 Insert Replacing WNV Insert in VR6430
US-11-131-479-101

Query Match 59.0%; Score 457; DB 12; Length 5161;
Best Local Similarity 75.0%; Pred. No. 6.8e-90;
Matches 571; Conservative 0; Mismatches 190; Indels 0; Gaps 0;
Qy 11 ATGAGCCTGTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCCTG 70
Db 1147 ATGAGCCTTCTAACCGAGGTGCAACGATGTCTCTATCGTTCCATCAGGCCCTC 1206
Qy 71 AAGCCGAGATCGCCAGAGCGCTGGAGGACGTGTTCGCCGCAAGAACACCGACTCGAG 130
Db 1207 AAAGCCGAATTCGGCAGAGACTTGAAGATGTCTTTGCTGGGAAAAACAGATCTTGAG 1266
Qy 131 GTGCTGATGGAGTGGCTGAAGACCCAGGCCCATCTCTGAGCCCTTGACCAAGGGCATCTG 190
Db 1267 GCTCTCATGAAATGGCTAAAGACCAAGCAATCTCTGACCTCTGACTAAGGGGATTTG 1326
Qy 191 GGCTTGTGTTTACCGTGCACCGTGCAGCGCGGCTGAGCGCGCGCTTCGTG 250
Db 1327 GGGTTGTGTTTACCGTGCACCGTGCAGCGCGGCTGAGCGGAGCTGCGAGCGTAGACGCTTGTG 1386
Qy 251 CAGAACGCCCTGAACGGCAACGGCGACCCCAACCAATGACAGAGGCGCTGAAGCTGTAC 310
Db 1387 CAAATGCCCTCAATGGGAATGGGGATCCAAATACATGACAGAGCAGATTAACTATAT 1446
Qy 311 AGGAAGCTGAAGAGGGAGATCACCTTCCAGCGGCCCAAGGAGATCAGCCTGAGCTACAGC 370
Db 1447 AGAAAACCTTAAGAGGGAGATTACATTTCCATGGGGCCAAAGAAATAGCACTCAGTTATTCT 1506

Qy 371 GCCGCGCCCTGGCCAGCTGATGGCCCTGATCTAACACAGATGGGCGCCGCTGACCACC 430
Db |||||
1507 GCTGGTGACATTGCCAGTTGCATGGCCCTCATATACACAGATGGGGGCTGTAACTACT 1566
Qy 431 GAGGTGGCTTCGGCCCTGGTGGCCACCTGGCGAGCAGATGCGGCAGCAGCAGCCGC 490
Db |||||
1567 GAAAGTGGCCCTTTGGCCCTGGTATGTGCAACATGTGAACAGATTTGCTGACTCCCGACACAGG 1626
Qy 491 AGCCACAGCGAGATGGTCACACACACCAACCCCTGATCAGGCGAGAGACAGGATGGTG 550
Db |||||
1627 TCTCATAGGCAATGGTGGCAACCAACCAATCATTAATAGGCATGAGAACAGATGGTT 1686
Qy 551 CTGGCCAGCACACCGCCCAAGGCCATGGAGCAGATGGCCGCGCAGCAGCAGCGCCGCC 610
Db |||||
1687 TTGGCCAGCACTACAGCTAAGCTATGGAGCAATGGCTGATCAAGTGAGCAGCAGCG 1746
Qy 611 GAGGCCATGAGGTGGCCAGCCAGCCAGGAGATGGTGAGGCGCATGAGGACCATCGGC 670
Db |||||
1747 GAGGCCATGGAATTTGCTAGTCAGGCCAGGCAATGGTGCAAGCAATGAGAGCCATTGGG 1806
Qy 671 ACCACCCACAGCAGCGCCGCTGAGAACGACCTGCTGGAGAACCTTCAGGCCCTAC 730
Db |||||
1807 ACTCATCTAGCTCCAGTGGCTGCTTAAAGATGATCTTCTTGAANAATTTGCAGACCTAT 1866
Qy 731 CAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
Db |||||
1867 CAGAAACGAATGGGGTGCAATGCACGATTTCAAGTGACC 1907

RESULT 14

US-11-131-479-91
; Sequence 91, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 91
; LENGTH: 5398
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4756, Ligation of Segment7 into VR10551
US-11-131-479-91

Query Match 59.0%; Score 457; DB 12; Length 5398;
Best Local Similarity 75.0%; Pred. No. 6.8e-90;
Matches 571; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

Qy 11 ATGAGCCTGCTGACCGAGGTGAGACCTACCTGCTGAGCATATCCCGAGCGCCCTG 70
Db |||||
1652 ATGAGCCTTCAACCGAGGTGGAACAGTATGTTCTCTATGTTCCATGAGGCCCCCTC 1711
Qy 71 AAGGCCGAGATCGCCAGAGGCTGGAGGACGTGTTGCGCGCAAGAACACCGACCTGGAG 130
Db |||||
1712 AAAGCCGAATCGCGCAGAGACTTGAAGATGCTTTGCTGGGAAAACACAGATCTTGAG 1771
Qy 131 GTGCTGATGGATGGCTGAAGACAGCGCCCATCTCTGAGCCCTTCGACCAAGGGATCTGT 190
Db |||||
1772 GCTCTCTGGAATGGCTAAAGACAGCAACCAATCTCTGTCACCTCTGACTAAGGGGATTTTG 1831

Qy 191 GGCTTCGTGTTTACCTTGACCGTGCACGAGCGCGCCCTGACGCGCGCCGCTTCGTG 250
Db |||||
1832 GGGTTTGTGTTTACGCTCACCGTGCCCGTGCAGCGAGGACTGCGAGCGTAGACGCTTTGTC 1891
Qy 251 CAGAACCCCTGAAGCGCAACGGCGACCCCAACAACATGCAAGGCGCGTGAAGCTGTAC 310
Db |||||
1892 CAAATGCCCTCAATGGGNAATGGGGATCCAAATTAACATGGACAGACAGTAAACTATAT 1951
Qy 311 AGGAAGCTGAAGAGGGAGATCACCTTCCAGCGCCCAAGGAGATCAGCTTCAGCTTACAGC 370
Db |||||
1952 AGAAAACTTAAGAGGAGATTAATTCATGGGGCCAAAGAAATAGCACTCAGTTATCT 2011
Qy 371 GCCGCGCCCTGGCCAGCTGCATGGGCTGATCTACAACAGATGGGCGCCGTGACCAACC 430
Db |||||
2012 GCTGGTGCACTTGCACGTTGCATGGGCTCATATAACAAGAAATGGGGCTGTAACCACT 2071
Qy 431 GAGGTGGCTTCGGCCCTGGTGTGGCCACCTGCGAGCAGATCGCGGACAGCAGCAGCCGC 490
Db |||||
2072 GAAGTGGCCCTTTGGCCCTGGTATGTGCAACATGTGAACAGATTTGCTGACTCCCGACACAGG 2131
Qy 491 AGCCACAGGCGAGATGGTGACCCACCACCAACCCCTGATCAGGCGACGAGAACAGGATGGT 550
Db |||||
2132 TCTCATAGGCAATGGTGGCAACCAACCAATCATTAATAGGCGATGAGAACAGATGGTT 2191
Qy 551 CTGGCCAGCACACCGCCAAAGGCCATGGAGCAGATGGCCGCGCAGCAGCAGCGCCGCC 610
Db |||||
2192 TTGGCCAGCACTACAGCTAAGGCTATGGAGCAATGCTGATCAAGTGAGCAGCAGCG 2251
Qy 611 GAGGCCATGAGGTGGCCAGCCAGGCGCAGGAGATGGTGAGGCCATGAGGACCATCGGC 670
Db |||||
2252 GAGGCCATGGAATTTGCTAGTCAGGCCAGGCAATGGTGCAGGCAATGAGAGCCATTGGG 2311
Qy 671 ACCACCCACAGCAGCAGCGCGCTGAGAACGACCTGCTGGAGAACCTTCGAGGACCTTAC 730
Db |||||
2312 ACTCATCTAGCTCCAGTGGTCTTAAAGATGATCTCTTTGAAAATTTTCAGACCTAT 2371
Qy 731 CAGAAGCGCATGGGCGTGCAGATGCAGCGCTTCAAGTGAAC 771
Db |||||
2372 CAGAAACGAATGGGGTGCAATGCACGATTTCAAGTGACC 2412

RESULT 15

US-11-131-479-97
; Sequence 97, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 97
; LENGTH: 7798
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4766, Ligation of Seg7 into VR4762
US-11-131-479-97

Query Match 59.0%; Score 457; DB 12; Length 7798;
Best Local Similarity 75.0%; Pred. No. 6.7e-90;
Matches 571; Conservative 0; Mismatches 190; Indels 0; Gaps 0;
Qy 11 ATGAGCCTGCTGACCGAGGTGAGACCTACGTGCTGAGCATCATCCCGAGCGGCCCTG 70

||||| ATGAGCCTTCTAAACCGAGGTCGAAACGTATGTTCTCTCTATCGTTCCATCAGGCCCCCTC 6152
Db
71 AAGGCCGAGATCGCCGAGAGCTCGAGGACGTGTTCCGCCGCAAGAACACCGACCTGGAG 130
Qy
6153 AAAGCCGAATCGCGCAGAGACTTGAAGATGTTCTTGTCTGGAAANAACAGATCTTGAG 6212
Db
131 GTGCTGATGAGTGGCTGAAGACACAGGCCCATCTGAGCCCTCTGACCAAGGGGATCCTG 190
Qy
6213 GCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACTCTGACTAAGGGGATTTTG 6272
Db
191 GGCTTCGTGTTCACTCGTCGCTGAGCGGTCGAGCGCGCTGACGCGCGCTTCGTG 250
Qy
6273 GGGTTTGTGTTACGCTCACCGTCCCGAGTGAGGAGACTGACGCGTAGACGCTTTGTC 6332
Db
251 CAGAAACCCCTGAAACGGCAACGGGAGCCCAACCAACATGGAACAAGGCCGTGAAGCTGTAC 310
Qy
6333 CAAATGCCCTCAATGGGAATGGGATCCAAATTAACATGGACAGCAGTTAACTATAT 6392
Db
311 AGAAGCTGAAGAGGAGATCACCTTCCAAGGCCCAAGGAGATCAGCCTGAGCTACAGC 370
Qy
6393 AGAAACCTTAAGAGGAGATTACATTCATGGGGCCAAAGAAATAGCACTCAGTTATTCT 6452
Db
371 GCCGCGCCCTGGCAGCTGATGGGCTGATCTACACAGGATGGGCGCTGACCAAC 430
Qy
6453 GCTGGTGCACTTGCACGTTGCATGGGCTCATATACAAAGAAATGGGGGCTGTAAACCACT 6512
Db
431 GAGTGGCCTTTGGCCTGGTGTGGCCACCTGCGAGCAGATCGCCGACAGCCAGCACCGC 490
Qy
6513 GAAGTGGCCTTTGGCCTGGTATGTGCAACATGTGACAGATTGCTGACTCCACGACAGG 6572
Db
491 AGCCACAGGCAAGTGGTGACCAACCAACCCCTGATCAGGCAAGAGAACAGGATGGTG 550
Qy
6573 TCTCATAGGCAAAATGGTGGCAACCAACCAATCCATTAAAGGCATGAGAACAGAAATGGTT 6632
Db
551 CTGGCCAGCACCAACCGCCAGGCCATGGAGCAGATGGCCGACAGCGAGCAGCGCCGCC 610
Qy
6633 TTGGCCAGCACTACAGCTAAGGCTATGGAGCAAAATGGCTGGATCAAGTGAGCAGGACGCG 6692
Db
611 GAGGCCATGAGGTGGCCAGCCAGGCAGAGATGGTGCAAGGCCATGAGGACCATCGGC 670
Qy
6693 GAGGCCATGGAATTTGCTAGTCAGGCCAGGCAAAATGGTGCAAGCCAATGAGAGCCATTGGG 6752
Db
671 ACCCACCCAGCAGCGCGGCTGAAAGAACGACCTGTGAGAACCTTCAGGCGCTAC 730
Qy
6753 ACTCATCTAGCTCCAGTGTGGTCTAAAGAGATGATCTTCTTGAATAATTCAGACCTAT 6812
Db
731 CAGAAGCGCATGGGGTGCAGATGCAGCGCTTCAAGTGAAC 771
Qy
6813 CAGAAACGAATGGGGGTGCAGATGCAACGATTCAAGTGACC 6853
Db

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GenCore version 5.1.7
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(without alignments)
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Perfect score: 844
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PCFUS COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	479.6	56.8	4023	3	US-08-809-513A-8
2	479.6	56.8	6802	3	US-08-809-513A-6
3	477.6	56.6	1023	3	US-08-506-286B-1
4	477.6	56.6	1023	3	US-09-762-861B-1
5	477.6	56.6	1023	3	US-10-065-133A-1
6	477.6	56.6	1023	3	US-10-434-811A-1
7	477.4	56.6	816	3	US-09-311-784A-13
8	474.8	56.3	1023	3	US-09-506-286B-4
9	474.8	56.3	1023	3	US-09-762-861B-4
10	474.8	56.3	1023	3	US-10-065-133A-4
11	474.8	56.3	1023	3	US-10-434-811A-4
12	474.2	56.2	756	3	US-09-506-286B-3
13	474.2	56.2	756	3	US-09-762-861B-3
14	474.2	56.2	756	3	US-10-065-133A-3
15	474.2	56.2	756	3	US-10-434-811A-3
16	471.4	55.9	756	3	US-09-506-286B-6
17	471.4	55.9	756	3	US-09-762-861B-6
18	471.4	55.9	756	3	US-10-065-133A-6
19	471.4	55.9	756	3	US-10-434-811A-6
20	465.2	55.1	1027	6	PCT-US95-12357A-3
21	79.2	9.4	2403	2	US-08-471-033-30
22	79.2	9.4	2403	2	US-08-471-044-30
23	79.2	9.4	2403	2	US-08-463-483A-30
24	79.2	9.4	2403	2	US-08-471-046A-30

25	79.2	9.4	2403	2	US-08-470-566B-30	Sequence 30, Appl
26	79.2	9.4	2403	2	US-08-838-219B-7	Sequence 7, Appl
27	79.2	9.4	2403	2	US-08-469-334-30	Sequence 30, Appl
28	79.2	9.4	2403	3	US-09-300-529-30	Sequence 30, Appl
29	79.2	9.4	2403	3	US-09-233-336A-7	Sequence 7, Appl
30	79.2	9.4	2403	3	US-09-233-752A-7	Sequence 7, Appl
31	79.2	9.4	2403	3	US-09-402-036-7	Sequence 7, Appl
32	79.2	9.4	2403	3	US-09-904-226-7	Sequence 7, Appl
33	77.8	9.2	1387	3	US-09-475-515-34	Sequence 34, Appl
34	77.8	9.2	1944	3	US-09-475-515-37	Sequence 37, Appl
35	77.8	9.2	1944	3	US-09-475-515-38	Sequence 38, Appl
36	77.8	9.2	1944	3	US-09-475-515-40	Sequence 40, Appl
37	77.8	9.2	1944	3	US-09-475-515-43	Sequence 43, Appl
38	77.8	9.2	1944	3	US-09-475-515-46	Sequence 46, Appl
39	77.8	9.2	2466	3	US-09-475-515-49	Sequence 49, Appl
40	77.8	9.2	4608	3	US-09-475-515-76	Sequence 76, Appl
41	77.6	9.2	2241	2	US-08-838-219B-20	Sequence 20, Appl
42	77.6	9.2	2241	3	US-09-233-336A-20	Sequence 20, Appl
43	77.6	9.2	2241	3	US-09-233-752A-20	Sequence 20, Appl
44	77.6	9.2	2241	3	US-09-402-036-20	Sequence 20, Appl
45	77.6	9.2	2241	3	US-09-904-226-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-809-513A-8
; Sequence 8, Application US/08809513A
; Patent No. 6524588
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
; TITLE OF INVENTION: Method
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NORRIS McLAUGHLIN & MARCUS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Gateway Pentium II
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,513A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03663
; FILING DATE: 18-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94115505.3
; FILING DATE: 30-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Hobom 9832-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4023 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO


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Db 401 GGTGCACTTGCAGTTGTATGGGCTCATATACAACAGGATGGGGCTGTGACCACTGAA 460
Qy 503 GTGGCTTCGCGCTGGTGTGCGCACCTGCGAGCAGATCGCGCAGCCAGCCAGCGCAGC 562
Db 461 GTGGCAITTTGGCTTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCAGCATCGGTCT 520
Qy 563 CACAGGAGATGGTGACCAACCAACCCCTGTATCGAGCAGAGAACAGGATGGTGTG 622
Db 521 CATAGGCAAAATGGTGACAAACCAACCAACCACTAATCAGACATGAGAACAGAAATGTTT 580
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Qy 683 GCCATGAGGTGGCCAGCCAGCCAGGAGATGGTGAGGCGCATGAGGACCATCGGCACC 742
Db 641 GCCATGAGGTGGCTAGTGCAGGCTAGGCAGGATGGTGAGGCGATGAGAACCATTTGGGACT 700
Qy 743 CACCCAGCAGCAGCGCGGCTGAAGAACGACCTGTCTGGAGAACCTGCGAGGCCCTACCA 802
Db 701 CATCTAGCTCAGTGTGCTGAAATAATGCTCTTCTTGAATAATTTGCGAGGCTATCAG 760
Qy 803 AAGCGCATGGCGTGCAGATGACGCGTTCAAGTGAAC 840
Db 761 AAACGAATGGGGTGCAGATGCAACGGTTCAAGTGATC 798

RESULT 3
US-09-506-286B-1
; Sequence 1, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: The University of Pittsburgh, of the Commonwealth
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION: At location 663, r = A or G; At amino acid
; OTHER INFORMATION: location 213, Xaa = Val
US-09-506-286B-1

Query March 56.6%; Score 477.6; DB 3; Length 1023;
Best Local Similarity 76.8%; Pred. No. 3.6e-80;
Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;

Qy 83 AGCTGTCTGACCGAGGTGGAGACCTACGTGTGTGAGCATATCCCGAGCGGCCCTCGAAG 142
Db 28 AGTCTTCTGACCGAGGTGCAACGTACGTTCTCTCTATCTGATCATCGGCCCTCMAA 87
Qy 143 GCCGAGATCGCCAGAGCTGGAGAGCGTGTTCGCCGCAAGAACACCGACCTCGAGGTG 202
Db 88 GCCGAGATCGCGAGAGACTTGAAGATGCTCTTTCAGGGAAGAACACCGATCTTTGAGGCA 147
Qy 203 CTGATGAGTGGCTGAAGACAGGCGCCATCTCTGAGCCCTTGACAGGAGGATCTCTGGC 262
Db 148 CTCATGGAATGGCTAAAGACAGACCAATCTCTGATCTGCTGACTAAAGGATTTAGGA 207
Qy 263 TTCGTGTTTACCTGACCGTGCCTCCCGAGCGCGGCTGCGAGCGCGGCTTCTGTGAC 322
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Db 268 AATGCCCTTATGTGAAACCGGAGATCCAAAACAAATGGACAGAGCAGTAAACCTGTACAGG 327
Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGCGCCAAAGAGATCAGCCTGAGCTACAGGCC 442
Db 328 AAGCTTAAAGAGAAATAACATTTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387
Qy 443 GGGCCCTGCGCAGCTGCTGATGGGCTGATCTCAACAGAGATGGGCGCGGTGACCAACCGAG 502
Db 388 GGTGCACTAGCCAGCTGCTGAGTGGACTCATATACAACAGAAATGGGAACTGTGACAACGAA 447
Qy 503 GTGGCTTCGCGCTGGTGTGCGCACCTGCGAGCAGATCCCGACAGCCAGCAGCCGAGC 562
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Qy 563 CACAGGAGATGGTGACCAACCAACCCCTGTATCAGGCAAGAGAACAGAGATGGTGTG 622
Db 508 CACAGGAGATGGTGACCAACCAACCCCTAATCAGATGNAACAGAAATGGTATTA 567
Qy 623 GCCAGCACCGCCAGGCGCATGAGCAGATGGCGGCAGCAGCGAGCGCGCCGAG 682
Db 568 GCCAGTACCACCGCTAAAGCCATGGAGCAGATGSCAGGGTCCAGTGAGCAGGCGCAGAG 627
Qy 683 GCCATGAGGTGGCGCAGCGCCAGGCGCAGATGGTGAGGCCCATGAGGACCATCGGCACC 742
Db 628 GCCATGAGGTGCTGTAGTAAAGCTTAGGCAGATGGTTCAGGCAATGAGAACCATTTGGGACC 687
Qy 743 CACCCAGCAGCAGCGCGGCTGAAGAACGACCTGTCTGGAGAACCTGCGAGGCGCTACCA 802
Db 688 CACCTAGCTCCAGTGGCGGTTTGAAGATGATCTCTTGAATAATTTGCGAGGCGCTACCA 747
Qy 803 AAGCGCATGGCGTGCAGATGACGCGTTCAAGTGAAC 840
Db 748 AAACGAATGGGAGTGCAAAATGCGAGCGATTCAGTGAATC 785

RESULT 4
US-09-762-861B-1
; Sequence 1, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS (formerly HK2-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-09-762-861B-1
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Query Match      56.6%; Score 477.6; DB 3; Length 1023;
Best Local Similarity 76.8%; Pred. No. 3.6e-80;
Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;

Qy 83 AGCTGCTGACCGAGGTGGAGACTAGTGTGCTGAGCATCATCCCGAGGCGCCCTCAAG 142
Db 28 AGTCTTCTGACCGAGGTGGAACGTAGCTTCTCTATCGTACCATCAGGCGCCCTCAA 87

Qy 143 GCCGAGATCGCCAGAGCTGGAGAGCTGTTCGCCGCGCAAGAACACCGACTGGAGTG 202
Db 88 GCCGAGATCGCGAGAGCTTGAAGATGTCTTTCAGGGAAGAACACCGATCTTGAGCA 147

Qy 203 CTGATGAGTGGCTGAAGACAGAGCCCATCTCAGAGCCCTGACCAAGGCGCATCTTGGC 262
Db 148 CTCATGATGGCTTAAAGACAAGACCAATCTCTGACCTCTGACTAAGGGATTTAGGA 207

Qy 263 TTGCTGTTACCCCTGACCGTCCAGCGAGCGCGCTTCAGCGCCCGCTTGTGTCAG 322
Db 208 TTGCTGTTACCGTCCAGCGTCCAGTGGAGGAGTGCAGCGTAGACGCTTGTCAA 267

Qy 323 AACGCCCTGAACCGCAACCGCGAGCCCAACATGAGCAAGCCGTGAAGCTGTACAGG 382
Db 268 AATGCCCTTAGTGGAAACCGGAGATCCAAACATGAGACAGAGCTGTAAACCTGTACAGG 327

Qy 383 AACGTGAAGAGGAGATCACCTTCCAGCGCGCAAGAGATCAGCTGAGCTACAGGCGC 442
Db 328 AAGCTTAAAGAGAAATTAACATTCATGGGGCAAGAGGTGGCACTCAGCTATTCCACT 387

Qy 443 GCGCCCTGCGAGCTGAGTGGCTGATCTCAACAGAGATGGCGCGCTGACCGCAG 502
Db 388 GGTGCACTAGCCAGCTGATGGGACTCATATACACAGAAATGGGAACTGTGACAAACGAA 447

Qy 503 GTGCGCTTGGCGCTGAGTGGCGGCGCTGAGAGAGATCGCGGAGCGAGCGCGCGAG 562
Db 448 GTGCGCTTGGCGCTGAGTGGCGGCGCTGAGAGAGATCGCGGAGCGAGCGCGAG 627

Qy 563 CACAGGAGATGGTGAACCAACCAACCCCTGATCGAGGCGCATGAGGACCATCGGCACC 742
Db 628 GCCATGGAGGTGTAGTAAAGCTAGGCGATGGTRCAGGCAATGAGAACCATTTGGGACC 687

Qy 743 CACCCAGCAGCGCGCGCTGAAAGAACGACCTGTCTGGAGAACCTGCGAGGCGCTACAG 802
Db 688 CACCCAGCAGCGCGCGCTGAAAGAACGACCTGTCTGGAGAACCTGCGAGGCGCTACAG 747

Qy 803 AAGCGATGGCGTGCAGATCAGCGCTTCAAGTGAAC 840
Db 748 AAACGGATGGAGTGCAAAATGCAGCGATTCAAGTGATC 785
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RESULT 5

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US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065.133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
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; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, xaa = Val
US-10-065-133A-1
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Query Match      56.6%; Score 477.6; DB 3; Length 1023;
Best Local Similarity 76.8%; Pred. No. 3.6e-80;
Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;

Qy 83 AGCTGCTGACCGAGGTGGAGACTAGTGTGCTGAGCATCATCCCGAGGCGCCCTCAAG 142
Db 28 AGTCTTCTGACCGAGGTGGAACGTAGCTTCTCTATCGTACCATCAGGCGCCCTCAA 87

Qy 143 GCCGAGATCGCCAGAGCTGGAGAGCTGTTCGCCGCGCAAGAACACCGACTGGAGTG 202
Db 88 GCCGAGATCGCGAGAGCTTGAAGATGTCTTTCAGGGAAGAACACCGATCTTGAGCA 147

Qy 203 CTGATGAGTGGCTGAAGACAGAGCCCATCTCAGAGCCCTGACCAAGGCGCATCTTGGC 262
Db 148 CTCATGATGGCTTAAAGACAAGACCAATCTCTGACCTCTGACTAAGGGATTTAGGA 207

Qy 263 TTGCTGTTACCCCTGACCGTCCAGCGAGCGCGCTTCAGCGCCCGCTTGTGTCAG 322
Db 208 TTGCTGTTACCGTCCAGCGTCCAGTGGAGGAGTGCAGCGTAGACGCTTGTCAA 267

Qy 323 AACGCCCTGAACCGCAACCGCGAGCCCAACATGAGCAAGCCGTGAAGCTGTACAGG 382
Db 268 AATGCCCTTAGTGGAAACCGGAGATCCAAACATGAGACAGAGCTGTAAACCTGTACAGG 327

Qy 383 AACGTGAAGAGGAGATCACCTTCCAGCGCGCAAGAGATCAGCTGAGCTACAGGCGC 442
Db 328 AAGCTTAAAGAGAAATTAACATTCATGGGGCAAGAGGTGGCACTCAGCTATTCCACT 387

Qy 443 GCGCCCTGCGAGCTGAGTGGCTGATCTCAACAGAGATGGCGCGCTGACCGCAG 502
Db 388 GGTGCACTAGCCAGCTGATGGGACTCATATACACAGAAATGGGAACTGTGACAAACGAA 447

Qy 503 GTGCGCTTGGCGCTGAGTGGCGGCGCTGAGAGAGATCGCGGAGCGAGCGCGCGAG 562
Db 448 GTGCGCTTGGCGCTGAGTGGCGGCGCTGAGAGAGATCGCGGAGCGAGCGCGAG 627

Qy 563 CACAGGAGATGGTGAACCAACCAACCCCTGATCGAGGCGCATGAGGACCATCGGCACC 742
Db 508 CACAGGAGATGGTGAACCAACCAACCCCTGATCGAGGCGCATGAGGAGCAATGAGAACCATTTGGGACC 687

Qy 623 GCCAGCACCAACCGCGAGGCGCATGGAGAGATGGCGGCGAGCGAGCGCGCGAG 682
Db 568 GCCAGTACCAACCGCTAAAGCCATGGAGCAGATGGCAGGGTCCGAGTGGAGCGAGCAGAG 627

Qy 683 GCCATGGAGGTGGCGAGCGCGCATGAGTGGCGGCGCATGAGGACCATCGGCACC 742
Db 628 GCCATGGAGGTGTAGTAAAGCTAGGCGATGGTRCAGGCAATGAGAACCATTTGGGACC 687

Qy 743 CACCCAGCAGCGCGCGCTGAAAGAACGACCTGTCTGGAGAACCTGCGAGGCGCTACAG 802
Db 688 CACCCAGCAGCGCGCGCTGAAAGAACGACCTGTCTGGAGAACCTGCGAGGCGCTACAG 747

Qy 803 AAGCGATGGCGTGCAGATCAGCGCTTCAAGTGAAC 840
Db 748 AAACGGATGGAGTGCAAAATGCAGCGATTCAAGTGATC 785
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US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-CI-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (663)..(663)
; OTHER INFORMATION: At nucleotide 663, r = a or g
; OTHER INFORMATION: At amino acid residue 213, xaa = Val
US-10-434-811A-1

Query Match 56.6%; Score 477.6; DB 3; Length 1023;
Best Local Similarity 76.8%; Pred. No. 3.6e-80;
Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;
Qy 83 AGCTGTGACCGAGGTGGAGACCTACGTGTGAGCATATCCCGAGCGGCCCTGAG 142
Db 28 AGTCTTCTGACCGAGGTGGAACGTACGTTCTCTATCATCATGAGCGGCCCTCAA 87
Qy 143 GCCGAGATCGCCAGAGCTGGAGCGTGTTCGGCGGCAAGAACACCGACCTGGAGTG 202
Db 88 GCCGAGATCGCGAGAGACTTGAAGATGTTTTCGAGGGAAGAACACCGATCTTGAGCA 147
Qy 203 CTGATGGAGTGGCTGAAGACAGGCGCCATCTCTGAGCGCCCTTGACCAAGGGCATCTGGGC 262
Db 148 CTCATGGAATGGCTAAAGACAAGACCAATCTGTCACTCTGACTAAAGGGATTTAGGA 207
Qy 263 TTCGTGTTACCTGACCGTGGCCAGCGAGCGCGCTGACGCGCGCTTGTGCGAG 322
Db 208 TTCGTATTTACGCTCACCGTGGCCAGTGGAGGAGCTGCGAGCGTGTGTCGCGT 267
Qy 323 AACGCTTGAAGCGCAAGCGGACCCCAACCAATGGAACAGGCGGTGAAGCTGTACAGG 382
Db 268 AATGCCCTTAGTGGAAACGGAGATCCAAACCAATGACAGACAGGATTAAGCTGTACAGG 327
Qy 383 AAGCTTGAAGAGGAGATCACCTTCCACGCGCGCCAGGAGATCAGCTGAGCTACAGCGCC 442
Db 328 AAGCTTAAAGAGAATAAATTCATTCATGGGCAAGAGGTGGCACTCAGCTATTCCACT 387
Qy 443 GCGCGCTTGGCGAGCTGATGGGCTGATCTTAAACAGGATGGGCGCGCTGACCAACCGAG 502
Db 388 GGTGCACTAGGCGAGCTGTGGGACTCATATACAGAAATGGGAACTGTGACCAACCGAA 447
Qy 503 GTGGCTTTCGCGCTGTGCGCACCTGCGGAGAGATCGCGGACAGCGCAGCGCAGC 562
Db 448 GTGGCAATTTGGCTGTGATGGCGCACATGTGAACAGATCGCTGATTCACGATCGATCT 507
Qy 563 CACAGGAGATGGTGACCAACCAACCCCTGTATCAGGCAACGAGATGGTGTG 622

Db 508 CACAGGAGATGGTGAACAACAACCAACCCATTAAATCAGACATGAAAAAGAGATGTATTA 567
Qy 623 GCCAGCACACCGCCAGAGCCATGGAGCAGATGSCCGGAGCAGCAGCAGGCGCCGAG 682
Db 568 GCCAGTACCACGGCTAAAGCCATGAGCAGATGGCAGGGTTCGAGTGAGCAGCAGAG 627
Qy 683 GCCATGAGGTGGCGAGCCAGGCGCAGATGGTGCAGGCCATGAGGACCATCGGACCC 742
Db 628 GCCATGAGGTTCCTAGTAAGGCTAGGCAGATGGTTCAGGCAATGAGAACCATTTGGGACC 687
Qy 743 CACCCAGAGCAGCGCGCCCTGAAGAACGACCTGTGAGGAGACCTGCGAGGCCCTACCG 802
Db 688 CACCTAGCTCCAGTGCCTGTTTGAAGAGATGATCTCCTTGAATAATTTGCGAGGCCCTACCG 747
Qy 803 AAGCGCATGGCGTGACAGATGACGCGCTTCAAGTGAAC 840
Db 748 AACCGATGGAGTGCAAAATGACGCGATTCAAGTGATC 785

RESULT 7
US-09-311-784A-13
; Sequence 13, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-2022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
; of pan DR epitope sequence to amino-terminus of
; OTHER INFORMATION: Influenza matrix protein gene
; NAME/KEY: CDS
; LOCATION: (16)..(816)
; OTHER INFORMATION: PADRE-Influenza matrix
US-09-311-784A-13

Query Match 56.6%; Score 477.4; DB 3; Length 816;
Best Local Similarity 75.6%; Pred. No. 3.8e-80;
Matches 592; Conservative 0; Mismatches 191; Indels 0; Gaps 0;
Qy 56 GCCCTGCGCCCTGACCCAGACCTGGGCTAGCTGTGACCCAGGTGGAGACCTAGTGTCTG 115
Db 34 GCCTGGACCTCGAAGGCTGCGCTATGAGTCTTTCTAACCGAGGTGCGAACGTAGCTTCTC 93
Qy 116 AGCATCATCCCCAGCGGCCCTTGAAGGCCGAGATGCCGAGAGCTGGAGGAGCGTGTTC 175
Db 94 TCTATCATCCATCAGGCCCCCTCAAGCCGAGATCGCGCAGAGACTTGGAGATGTTTTT 153
Qy 176 GCGCGCAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACAGCCAGCCCATCTG 235
Db 154 GCAGGGAAGAACACAGATCTTGGAGTCTCATGSAATGGCTAAAGACAAGACCAATCTG 213
Qy 236 AGCCCCCTGACCAAGGGCATCTCGGGCTTGTGTTTACCCCTGACCGTGCAGGCGGAGCGC 295
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; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
US-09-762-861B-4

Query Match          56.3%; Score 474.8; DB 3; Length 1023;
Best Local Similarity 76.6%; Pred. No. 1.2e-79;
Matches 581; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

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Qy 28 AGTCTTCTGACCGAGGTGGAAGTACGTTCTCTATCTTACCATCAGGCCCTCAA 87
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Qy 143 GCCGAGATCGCGCAGAGCTGGAGACGTGTTGCGCGCAAGAACACCGACCTGAGGTG 202
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 88 GCCGAGATCGCGCAGAGCTTGAAGATGTTCTTGTACGAGGAAACACCGATCTTGAGGCA 147
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 203 CTGATGGAGTGGCTGAAGACGAGCCCATCTGAGCCCCCTGACCAAGGGCATCTGGGC 262
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 148 CTCATGGAATGGCTTAAGACCAAGACCANTCTGTCACTCTGACTTAAGGGATTTAGGA 207
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 263 TTGCTGTTCACTTACCGTGCAGCGAGCGCGCTGACGCGCGCGCTTGTGCGAG 322
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 208 TTGCTATTACGCTCACCGTCCAGTGCAGTGCAGGAGCTGCAGCGTAGACGCTTTGCCAA 267
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 323 AACGCCCTGAAGCGGCAAGCGGACCCCAACATGGAACAGGCGGTGAGCTGTACAGG 382
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 268 AATGCCCTTAGTGGAAACGGAGATCCAAACATGGAACAGAGCAGTAAACTGTACAGG 327
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGGCCAAGGAGATCAGCCTGAGCTACAGGCC 442
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 328 AAGCTTAAAGAGNAATTAATTCATGGGGCAAGAGGTGGCACTCAGCTATTCACCT 387
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 443 GCGCCCTTGGCCAGCTGCATGGGCTGATCTACAACAGGATGGCGCGCTGACCCGAG 502
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAAGAAATGGGAACTGTGACAACCGAA 447
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 503 GTGGCTTTCGGCTGGTGTGGCCACCTGCGAGCAGATCGCCGACAGCCAGCCAGCCGAG 562
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 448 GTGGCATTTGGCTGGTGTGGCCACATGTGNAACAGATCGCTGATTTCCCAAGCATCTGT 507
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 563 CACAGGCAGATGGTGACCAACCAACCCCTGATCAGGCACGAGAACAGAGTGGTGTG 622
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 508 CACAGGCAGATGGTGACAAATAACCAACCCATTATACAGATGNAACAGAAATGGTATTA 567
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 623 GCCAGCACCAACGCCCAAGGCCATGGAGCAGATGGCCGCGCAGCAGCGAGCCGCGAG 682
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 568 GCCAGTACCACGGCTTAAGCCATGGAGCAGATGGCAGGGTTCGAGTGCAGCGCAGCAGAG 627
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 683 GCCATGGAGGTGGCCAGCCAGCCAGGCGAGATGGTGCAGGCGCATGAGGACCATCGGCACC 742
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 628 GCCATGGAGGTGGTGTAGTGAAGGTAGGAGAGTGGTACAGGCAATGAGAAACCATTTGGGACC 687
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 743 CACCCACAGCAGCGCGGCTGAGAACGACCTGCTGAGAACCTTCAGGACCTTACCAG 802
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 688 CACCCTAGCTCCAGTGGCGGTTTGAAGAGATGATCTCTTTGAAAATTTTGACGGCTTACCAG 747
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 803 AAGCCATGGCGGTGCAGATGCAGCGCTTCAAGTGAAC 840
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 748 AAACGGATGGAGTGCAATGCAGCGATTCAAGTGATC 785
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 10
US-10-065-133A-4
; Sequence 4, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
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; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
US-10-065-133A-4

Query Match          56.3%; Score 474.8; DB 3; Length 1023;
Best Local Similarity 76.6%; Pred. No. 1.2e-79;
Matches 581; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

Qy 83 AGCCTGTGACCGAGGTGGAGACCTACGTGTGAGCATCATCCCGAGCGGCCCTGAAG 142
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 28 AGTCTTCTGACCGAGGTGGAAGTACGTTCTCTATCTTACCATCAGGCCCTCAA 87
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 143 GCCGAGATCGCGCAGAGCTGGAGACGTGTTGCGCGCAAGAACACCGACCTGAGGTG 202
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 88 GCCGAGATCGCGCAGAGACTTGAAGATGTTCTTGTACGAGGAAACACCGATCTTGAGGCA 147
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 203 CTGATGGAGTGGCTGAAGACGAGCCCATCTGAGCCCCCTGACCAAGGGCATCTGGGC 262
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 148 CTCATGGAATGGCTTAAGACCAAGACCANTCTGTCACTCTGACTTAAGGGATTTAGGA 207
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 263 TTGCTGTTCACTTACCGTGCAGCGAGCGCGCTGACGCGCGCGCTTGTGCGAG 322
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 208 TTGCTATTACGCTCACCGTCCAGTGCAGTGCAGGAGCTGCAGCGTAGACGCTTTGCCAA 267
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 323 AACGCCCTGAAGCGGCAAGCGGACCCCAACATGGAACAGGCGGTGAGCTGTACAGG 382
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 268 AATGCCCTTAGTGGAAACGGAGATCCAAACATGGAACAGAGCAGTAAACTGTACAGG 327
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGGCCAAGGAGATCAGCCTGAGCTACAGGCC 442
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 328 AAGCTTAAAGAGNAATTAATTCATGGGGCAAGAGGTGGCACTCAGCTATTCACCT 387
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 443 GCGCCCTTGGCCAGCTGCATGGGCTGATCTACAACAGGATGGCGCGCTGACCCGAG 502
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 388 GGTGCACTAGCCAGCTGCATGGGACTCATATACAAGAAATGGGAACTGTGACAACCGAA 447
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 503 GTGGCTTTCGGCTGGTGTGGCCACCTGCGAGCAGATCGCCGACAGCCAGCCAGCCGAG 562
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 448 GTGGCATTTGGCTGGTGTGGCCACATGTGNAACAGATCGCTGATTTCCCAAGCATCTGT 507
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 563 CACAGGCAGATGGTGACCAACCAACCCCTGATCAGGCACGAGAACAGAGTGGTGTG 622
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 508 CACAGGCAGATGGTGACAAATAACCAACCCATTATACAGATGNAACAGAAATGGTATTA 567
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 623 GCCAGCACCAACGCCCAAGGCCATGGAGCAGATGGCCGCGCAGCAGCGAGCCGCGAG 682
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 568 GCCAGTACCACGGCTTAAGCCATGGAGCAGATGGCAGGGTTCGAGTGCAGCGCAGCAGAG 627
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 683 GCCATGGAGGTGGCCAGCCAGCCAGGCGAGATGGTGCAGGCGCATGAGGACCATCGGCACC 742
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 628 GCCATGGAGGTGGTGTAGTGAAGGTAGGAGAGTGGTACAGGCAATGAGAAACCATTTGGGACC 687
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 743 CACCCACAGCAGCGCGGCTGAGAACGACCTGCTGAGAACCTTCAGGACCTTACCAG 802
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 688 CACCCTAGCTCCAGTGGCGGTTTGAAGAGATGATCTCTTTGAAAATTTTGACGGCTTACCAG 747
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 803 AAGCCATGGCGGTGCAGATGCAGCGCTTCAAGTGAAC 840
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 748 AAACGGATGGAGTGCAATGCAGCGATTCAAGTGATC 785
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 748 AACCGATGGAGTGCAATCCAGCGATTCAAGTGATC 785

RESULT 11
US-10-434-811A-4
; Sequence 4, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Youngner, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-CL-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
US-10-434-811A-4

Query Match 56.3%; Score 474.8; DB 3; Length 1023;
Best Local Similarity 76.6%; Pred. No. 1.2e-79;
Matches 581; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

Qy 83 AGCTGTGACCGAGGTGGAGACCTACGTGTGAGATCATCCCGAGGGCCCCCTGAAG 142
Db 28 AGTCTTCTGACCGAGGTGGAACGTACGTTCTCTATCTTACCATTACGAGCCCCCTCAA 87

Qy 143 GCCGAGATCGCCAGAGCTCGAGAGCTGTTCGCCGGAAGAACACCGACCTGGAGTG 202
Db 88 GCCGAGATCGCCGAGAGACTTGAAGATGTCTTTCGAGGAAGAACCGATCTTGAGGCA 147

Qy 203 CTGATGAGTGGCTGAAGACAGAGCCCATCTGTAGCCCTTGACCAAGGGCATCTGGGC 262
Db 148 CTCATGGAATGGCTAAAGACAAGACCAATCTGTCTGACCTCTGACTAAAGGGATTTAG 207

Qy 263 TTCGTGTTACCTGACCGTCCCGAGCGCGCCCTGACGCGCGCTTCGTGCAG 322
Db 208 TTCGTATTTACGCTCACCGTCCCGAGTGGCGGAGCTGCGAGCTTAGACGCTTTGTCAA 267

Qy 323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGAACAGGCGGTGAAGCTGTACAG 382
Db 268 AATGCCCTTAGTGMAACGGAGATCCAAACAACTGGACAGAGTAATAACTGTACAG 327

Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGCCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
Db 328 AAGCTTAAAGAGAAATAACATTTCCATGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387

Qy 443 GGGCCCTGGCAGCTGATGGGCTGATCTTACAACAGGATGGGCGCGTACACCCAG 502
Db 388 GGTGCATAGGCAGCTGATGGGACTCATATACAAAGATGGGAATGTGACAAACCGAA 447

Qy 503 GTGGCTTCGCGCTGTGCGCACCTCGAGCAGATCGCGGACAGCGACCGCAGC 562
Db 448 GTGGCATTTGGCTGTGATGGCCACATGTGAACAGATCGCTGATTCACGATCGATCT 507

Qy 563 CACAGGCAGATGGTGAACACCAACCCCTGTATCAGGACGAGAACAGGATGGTGTG 622
Db 508 CACAGGCAGATGGTGAACAAATTAACCAACCCATTAATATCAGACATGAATAAGATGTA 567

Qy 623 GCCAGCACCGCCAGGCTATGGAGCAGATGGCCGCGAGCAGCGAGCGCCCGAG 682

Db 568 GCCAGTACCAAGCGCTAAAGCCATGGAGCAGATGGCAGGCTCGAGTGAGCAGCAGAG 627

Qy 683 GCCATGGAGTGGCCAGCAGCCAGCCAGAGATGGTGCAGGCCATGAGGACCATCGGCACC 742

Db 628 GCCATGGAGTGGCTAGTAAGGCTAGGCAGATGGTACAGGCAATGAGAACCATTTGGACC 687

Qy 743 CACCCAGCAGCAGCGCCGCTGAAGACGACTCTGTGGAGAACCTGGAGGCTTACCAG 802

Db 688 CACCCTAGCTCCAGTCCCGGTTTGAAGAGATGATCTCTTGAATAATTTGCAGGCTTACCAG 747

Qy 803 AAGCGCATGGCTGCGAGATGCGAGCGCTTCAAGTGAAC 840

Db 748 AAACGATGGAGTGCAATGCGAGCGATTCAAGTGATC 785

RESULT 12
US-09-506-286B-3
; Sequence 3, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-3

Query Match 56.2%; Score 474.2; DB 3; Length 756;
Best Local Similarity 76.8%; Pred. No. 1.5e-79;
Matches 578; Conservative 1; Mismatches 174; Indels 0; Gaps 0;

Qy 83 AGCTGTGACCGAGGTGGAGACCTAGCTGTGAGCATCATCCCGAGGGCCCCCTGAAG 142
Db 4 AGTCTTCTGACCGAGGTGGAACGTACGTTCTCTATCTGATACCATCAGGCCCCCTCAA 63

Qy 143 GCCGAGATCGCCAGAGCTGGAGAGCTGTTCGCCGGAAGAACACCGACCTGGAGTG 202
Db 64 GCCGAGATCGCCGAGAGACTTGAAGATGTCTTTCGAGGAAGAACCCGATCTTGAGGCA 123

Qy 203 CTGATGAGTGGCTGAAGACAGCGCCCATCTGTAGCCCTTGACCAAGGCGATCTGGGC 262
Db 124 CTCATGGAATGGCTTAAGACAAGACCAATCTGTCTGACTCTGACTAAAGGGATTTAG 183

Qy 263 TTGCTGTTCACCTGTAGCTGCCAGCGCGCGCTGACGCGCCCGCTTCGTGCAG 322
Db 184 TTGCTATTACGCTCACCGTCCCGAGTGGAGGACTGCGAGCGTAGACGCTTTGTCAA 243

Qy 323 AACGCCCTGAACGGCAACGGCGACCCCAACAACATGGAACAGGCGGTGAAGCTGTACAG 382
Db 244 AATGCCCTTAGTGMAACGGAGATCCAAACAACTGGACAGAGTAATAACTGTACAG 303

Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGCCCAAGGAGATCAGCCTGAGCTACAGGCC 442
Db 304 AAGCTTAAAGAGAAATAACATTTCCATGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 363

Qy 443 GGGCCCTGGCAGCTGATGGGCTGATCTTACAAGGATGGGCGCGCTGACACCCAG 502
Db 364 GGTGCATAGGCAGCTGATGGGACTCATATACAAAGATGGGAATGTGACAAACCGAA 423

Qy 503 GTGGCTTCGCGCTGTGCGCACCTCGAGCAGATCGCCGCGAGCAGCGACCGCAGC 562

Db 424 GTGGCAATTTGGCTGTATGGCCACATGTGAACAGATCGTGAATTCACGATCGATCT 483
Qy 563 CACAGGAGATGGTACACACACACCCCTGTATTCATTCAGGACGAGATGGTGTG 622
Db 484 CACAGGAGATGGTACACACACACCCATTAATCAGACATGAACAGAAATGATTA 543
Qy 623 GCCAGCACACCGCCCAAGCCATGAGCAGATGGCCGCGCAGCAGCAGCGCCCGAG 682
Db 544 GCCAGTACACCGCTAAAGCCATGGAGCAGATGGCAGGTCGAGTGAGCAGCAGCAG 603
Qy 683 GCCATGAGATGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 742
Db 604 GCCATGAGATGGTGTAGTAAAGCTAGGAGATGGTTCAGGCAATGAGAACCAATTGGGACC 663
Qy 743 CACCCACAGCAGCAGCGCCGCTGAAGAACGACCTGCTGGAGAACCTTCAGGCCCTACCAG 802
Db 664 CACCCCTAGCTCCAGTGGCGGTTTGAAGATGATCTCTTGAATAATTTGAGGCCCTACCAG 723
Qy 803 AAGCCATGGCGCTGCAGATGCAGCGCTTCAAG 835
Db 724 AAACGGATGGAGTGCAAAATGCAGCGATTCAAG 756

RESULT 13

US-09-762-861B-3
; Sequence 3, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-CI-PUS (formerly HK2-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-762-861B-3

Query Match 56.2%; Score 474.2; DB 3; Length 756;
Best Local Similarity 76.8%; Pred. No. 1.5e-79;
Matches 578; Conservative 1; Mismatches 174; Indels 0; Gaps 0;
Qy 83 AGCTGTGACCGAGTGGAGACCTACGTGTGAGCATCATCCCGAGCGGCCCTGAAG 142
Db 4 AGTCTTCTGACCGAGTGCAGAAAGTACGTCTCTCTATCGTACCATCAGGCCCTCAA 63
Qy 143 GCCGAGATCGCCAGAGCTGGAGAGCTGTTCGCCGCAAGAACACCGACTGGAGTG 202
Db 64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGAGGGAAGAACACCGCATCTTGAGGCA 123
Qy 203 CTGATGGATGGCTGAAGACAGCCCATCTCTGAGCCCTGACGCGCGCGCTTCGTGAG 262
Db 124 CTCATGGAATGGCTTAAGACAGCAATCTCTGACCTCTGACTAAGAGGATTTAGGA 183
Qy 263 TTGCTGTTTCACTGACCGTGCACGAGCGCGCTGCAGCGCGCGCTTCGTGAG 322
Db 184 TTGCTGTTTCACTGACCGTGCACGAGCGCGCTGCAGCGCGCGCTTCGTGAG 243
Qy 323 AACGCCCTGAAGCGCAACCGGCCACCCCAACACATGGAACGAGCGGTGAGCTGACAG 382
Db 244 AATGCCCTTAGTGGAAACGGAGATCCAAACACATGGAACGAGCAGATGAACCTGTACAGG 303

Qy 383 AAGCTGAAGAGGGAGATCACCTTCCAGCGCCCAAGAGATCAACCTGAGCTACAGCGCC 442
Db 304 AAGCTTAAAGAGAAAATAACATTCATGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 363
Qy 443 GGCGCCCTGGCCAGCTGCATGGGCTGATCTACAAAGGATGGGCGCGCTGACACCGAG 502
Db 364 GGTGCACTAGCCAGCTGCATGGGACTCATATACACAGAAATGGGAACCTGTGACAAACGAA 423
Qy 503 GTGCGCTTGGCGCTGTGTGGCCACCTGCGAGCAGATCGCCGACAGCAGCAGCAGCGCAGC 562
Db 424 GTGCAATTTGGCTGTGTATGGCCACATGTGAACAGATCGCTGATTTCCAGCATCGATCT 483
Qy 563 CACAGGAGATGGTGAACACACCAACCCCTGTATCAGGACGAGAACAGATGGTGTG 622
Db 484 CACAGGAGATGGTGAACACCAACCCATTAATCAGACATGAACAGAAATGATTA 543
Qy 523 GCCAGCACACCGCCCAAGCCATGGAGCAGATGGCCGCGCAGCAGCAGCGCCCGAG 682
Db 544 GCCAGTACCAACCGCTAAAGCCATGGAGCAGATGGCAGGTCGAGTGAGCAGCGCAGCAG 603
Qy 683 GCCATGAGTGGCCAGCAGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 742
Db 604 GCCATGAGTGGCTAGTAGGCTAGGAGATGGTTCAGGCAATGAGAACCATTTGGGACC 663
Qy 743 CACCCACAGCAGCAGCGCCGCTGAAGAACGACCTGCTGGAGAACCTTCAGGCCCTACCAG 802
Db 664 CACCCCTAGCTCCAGTGGCGGTTTGAAGATGATCTCTTGAATAATTTGAGGCCCTACCAG 723
Qy 803 AAGCCATGGCGCTGCAGATGCAGCGCTTCAAG 835
Db 724 AAACGGATGGAGTGCAAAATGCAGCGATTCAAG 756

RESULT 14

US-10-065-133A-3
; Sequence 3, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-3

Query Match 56.2%; Score 474.2; DB 3; Length 756;
Best Local Similarity 76.8%; Pred. No. 1.5e-79;
Matches 578; Conservative 1; Mismatches 174; Indels 0; Gaps 0;
Qy 83 AGCTGTGACCGAGTGGAGACCTACGTGTGAGCATCATCCCGAGCGGCCCTGAAG 142
Db 4 AGTCTTCTGACCGAGTGCAGAAAGTACGTCTCTCTATCGTACCATCAGGCCCTCAA 63
Qy 143 GCCGAGATCGCCAGAGCTGGAGAGCTGTTCGCCGCAAGAACACCGACTGGAGTG 202
Db 64 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGAGGGAAGAACACCGCATCTTGAGGCA 123
Qy 203 CTGATGGATGGCTGAAGACAGCCCATCTCTGAGCCCTGACGCGCGCGCTTCGTGAG 262
Db 124 CTCATGGAATGGCTTAAGACAGCAATCTCTGACCTCTGACTAAGAGGATTTAGGA 183
Qy 263 TTGCTGTTTCACTGACCGTGCACGAGCGCGCTGCAGCGCGCGCTTCGTGAG 322

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Db 184 TTGCTATTACGCTCACCGTGCCAGTCAGTGAGGAGACTGACGCTTAGACGCTTTGTCCAA 243
Qy 323 AACGCCCTGAACGCAACGCGACCCCAACAACATGGACAGGCGGTGAAGCTGTACAGG 382
Db 244 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGGAGTAAACTGTACAGG 303
Qy 383 AAGCTGAAGAGGAGATCACCTTCACGGCGCCCAAGAGAGATCACCTTGAGCTACAGGCC 442
Db 304 AAGCTTAAAGAGAAATAAATTCATGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 363
Qy 443 GCGCCCTGCCAGCTGCATGGGCTGATCTACACAGGATGGGCGGTGACACCGAG 502
Db 364 GGTGCACTAGCCAGCTGCATGGGACTCATATACACAGAAATGGGAACTGTGACAACCGAA 423
Qy 503 GTGCGCTTGGCGCTGTGTGCGCCACCTGCGAGCAGATCGCGCAGCAGCACCGCAGC 562
Db 424 GTGCGATTGGCGCTGTGTGCGCCACATGTGAAACAGATCGCTGATTCAGCATCTCT 483
Qy 563 CACAGGAGATGTGTACACACCAACCCCTGTATCAGGACGAGAACAGGATGGTGTG 622
Db 484 CACAGGAGATGTGTGACAAACCAACCAATTAATCAGACATGAACAGAAATGGTATTA 543
Qy 623 GCCAGCACCCCGCAGGCGGCTGAAAGAACCACTGTGTGAGAACCTGCGAGGCTTACAG 802
Db 664 CACCCTAGCTCAGTGCCTGCGGTTTGAAGATGATCTCTTGAATAATTTGCAGGCTTACAG 723
Qy 803 AAGCGCATGGCGTGCAGATCAGCGCTTCAAG 835
Db 724 AAACGGATGGGAGTGCAAAATCAGCGATTCAAG 756

RESULT 15
US-10-434-811A-3
; Sequence 3, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-434-811A-3
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Query Match 56.2%; Score 474.2; DB 3; Length 756;
Best Local Similarity 76.8%; Pred. No. 1.5e-79;
Matches 578; Conservative 1; Mismatches 174; Indels 0; Gaps 0;

Qy 83 AGCTGTCTGACCGAGGTGGAGACCTTACGTGTGTGAGCATCATCCCCAGCGGCCCCCTGAAG 142
Db 4 AGTCTTCTGACCGAGGTGCAAAATCAGCGATTCTCTCTATCGTACCATCATGAGGCCCTCTCAA 63
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Qy 143 GCCAGATCGCCAGAGGCTGGAGGCTGTCTCGCGGCAAGAACACCGACCTGGAGGTG 202
Db 64 GCCAGATCGCGCAGAGACTTTGAAGATGTCTTTGCGGGGAAGAACACCGATCTTGAGGCA 123
Qy 203 CTGATGGAGTGGCTGAAGACACGAGCCCATCTCTGAGCGCCCTGACCAAGGGCATCTTGGGC 262
Db 124 CTCATGGAATGGCTTAAGACAAGACCAATCTCTGTACCTCTGTAAAGGATTTTAGGA 183
Qy 263 TTGCTGTTCACCTGACCGTGCAGGAGCGCGGCTGTGAGCGCCCGCTGCTGTGTCAG 322
Db 184 TTGCTATTACAGCTACCGTGCAGTGCAGGAGGACTGCGAGCGTAGACGCTTTGTCCAA 243
Qy 323 AAGCGCTTGAACGCAACGCGACCCCAACAACATGACACAGGCGGTGAAGCTGTACAGG 382
Db 244 AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAATTAACCTGTACAGG 303
Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGCGCCCAAGAGATCAGCTGTAGCTACAGGCC 442
Db 304 AAGCTTAAAGAGAAATAAATTCATGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 363
Qy 443 GCGCGCTTGGCGCTGATGTGCGGCTGATCTCAACAGGATGGGCGCGGTGACACCGAG 502
Db 364 GGTGCACTAGCCAGCTGCATGGGACTCATATACACAGAAATGGGAACTGTGACAACCGAA 423
Qy 503 GTGCGCTTGGCGCTGTGTGCGGCACTGCGAGCAGATCGCGCAGCAGCACCGCAGC 562
Db 424 GTGCGATTGGCGCTGTGTGCGGCACTGTGAAACAGATCGCTGATTCAGCATCTCT 483
Qy 563 CACAGGAGATGTGTACACCAACCCCTGTATCAGGACGAGAACAGGATGGTGTG 622
Db 484 CACAGGAGATGTGTGACAAACCAACCCATTAATCAGACATGAACAGAAATGGTATTA 543
Qy 623 GCCAGCACCCCGCAGGCGGCTGAGAGCAGATGGCGGCGAGCAGCGAGGCGCGCAG 682
Db 544 GCCAGTACCAACGCGTAAAGCCATGGAGCAGATGGCAGGCTCGAGTGCAGGCGAGCAGAG 603
Qy 683 GCCATGGAGGTGGCGGCGCAGCGGCGAGGCTGTGCGAGGCGCATGAGGACCATCGGCACC 742
Db 604 GCCATGGAGGTGTCTAGTAAGGCTTAGGCAGATGGTTCAGGCAATGAGAACCATTTGGGACC 663
Qy 743 CACCCAGCAGCAGCGCGCTGAAAGAACCACTGTGTGAGAACCTGCGAGGCTTACAG 802
Db 664 CACCTTAGCTCCAGTGCCTGCGGTTTGAAGATGATCTCTTGAATAATTTGCAGGCTTACAG 723
Qy 803 AAGCGCATGGCGTGCAGATCAGCGCTTCAAG 835
Db 724 AAACGGATGGGAGTGCAAAATCAGCGATTCAAG 756
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Search completed: March 20, 2006, 23:50:23
Job time : 173.124 secs

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OM nucleic - nucleic search, using sw model

Run on: March 20, 2006, 23:29:50 ; Search time 829.608 Seconds
(without alignments)
8412.838 Million cell updates/sec

Title: US-10-729-830-4
Perfect score: 844
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
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8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	844	100.0	844	8	US-10-729-830-4	Sequence 4, Appli
2	842.4	99.8	1011	8	US-10-729-830-7	Sequence 7, Appli
3	762	90.3	775	8	US-10-729-830-3	Sequence 3, Appli
4	762	90.3	942	8	US-10-729-830-6	Sequence 6, Appli
5	494	58.5	986	8	US-10-866-484-9	Sequence 9, Appli
6	486.8	57.7	942	8	US-10-729-830-5	Sequence 5, Appli
7	485.8	57.6	774	8	US-10-729-830-1	Sequence 1, Appli
8	481.2	57.0	1027	8	US-10-177-390-31	Sequence 31, Appli
9	478	56.6	1027	8	US-10-855-875-5	Sequence 5, Appli
10	477.6	56.6	1023	6	US-10-371-069-13	Sequence 13, Appli
11	477.6	56.6	1023	7	US-10-434-811A-1	Sequence 1, Appli
12	477.6	56.6	1023	7	US-10-734-373-1	Sequence 1, Appli
13	477.6	56.6	1023	8	US-10-872-014-1	Sequence 1, Appli
14	477.4	56.6	816	6	US-10-371-525-13	Sequence 13, Appli
15	477.4	56.6	816	6	US-10-371-069-13	Sequence 13, Appli
16	477.4	56.6	816	6	US-10-371-645-13	Sequence 13, Appli
17	477.4	56.6	816	6	US-10-371-260-13	Sequence 13, Appli
18	474.8	56.3	1023	6	US-10-065-133A-4	Sequence 4, Appli
19	474.8	56.3	1023	7	US-10-434-811A-4	Sequence 4, Appli
20	474.8	56.3	1023	7	US-10-734-373-4	Sequence 4, Appli
21	474.8	56.3	1023	8	US-10-872-014-4	Sequence 4, Appli
22	474.2	56.2	756	6	US-10-065-133A-3	Sequence 3, Appli
23	474.2	56.2	756	7	US-10-434-811A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-10-729-830-4
; Sequence 4, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 844
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: gene for secreted form (with N-terminal
; OTHER INFORMATION: signal sequence) with increased G/C-content
; FEATURE:
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
; OTHER INFORMATION: codon: tga (nucleotides 836 to 838)
US-10-729-830-4

Query Match 100.0%; Score 844; DB 8; Length 844;
Best Local Similarity 100.0%; Pred. No. 7.6e-190;
Matches 844; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGATCTAAAGATGGCGCTCATGGCCCCCGCACCCCTGGTGTGCTGTGCTGAGCGGCGCCT	60
Db	1	AGATCTAAAGATGGCGCTCATGGCCCCCGCACCCCTGGTGTGCTGTGCTGAGCGGCGCCT	60
Qy	61	GGCCCTGACCCAGACCTGGGCTAGCCTGTGCTGACCGAGGTGGAGACCTACGTTCTGAGCAT	120
Db	61	GGCCCTGACCCAGACCTGGGCTAGCCTGTGCTGACCGAGGTGGAGACCTACGTTCTGAGCAT	120
Qy	121	CATCCCCAGCGGCCCTCTGAAGCCGCGAGATCGCCAGAGGTGGAGACCTGTTTCGCGGG	180
Db	121	CATCCCCAGCGGCCCTCTGAAGCCGCGAGATCGCCAGAGGTGGAGACCTGTTTCGCGGG	180

; Sequence 3, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingrid
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; FILE OF INVENTION: Optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; TYPE: DNA
; LENGTH: 775
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: gene with increased G/C-content
; FEATURE:
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
; OTHER INFORMATION: codon: tga (nucleotides 767 to 769)
US-10-729-830-3

Query Match 90.3%; Score 762; DB 8; Length 775;
Best Local Similarity 100.0%; Pred. No. 1.8e-170;
Matches 762; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 83 AGCTGTGACCGAGGTGGAGACCTACGTGTGAGCATCATCCCGAGCGGCCCTGAAG 142
Db 14 AGCTGTGACCGAGGTGGAGACCTACGTGTGAGCATCATCCCGAGCGGCCCTGAAG 73
Qy 143 GCCGAGATGCGCAGAGCTGGAGAGCTGTTTCGCGCGCAAGAACACCGACCTGGAGTG 202
Db 74 GCCGAGATGCGCAGAGCTGGAGAGCTGTTTCGCGCGCAAGAACACCGACCTGGAGTG 133
Qy 203 CTGATGGATGGCTGAGACAGCGCCCATCTGTGAGCCCTTGACCAAGGGCATCTGGGC 262
Db 134 CTGATGGATGGCTGAGACAGCGCCCATCTGTGAGCCCTTGACCAAGGGCATCTGGGC 193
Qy 263 TTCGTGTTACCTTGACCGTCCAGCGAGCGCGCTGACGCGCGCGCTTGTGTGAG 322
Db 194 TTCGTGTTACCTTGACCGTCCAGCGAGCGCGCTGACGCGCGCGCTTGTGTGAG 253
Qy 323 AACGCCCTGAACGGCAACGGCGACCCCAACATGGAACAGGCGCGTGAAGCTGTACAGG 382
Db 254 AACGCCCTGAACGGCAACGGCGACCCCAACATGGAACAGGCGCGTGAAGCTGTACAGG 313
Qy 383 AAGCTGAGAGGGAGATCACCTTCCAGCGCGCGCGAGGATGACGCTGAGCTACAGCGCC 442
Db 314 AAGCTGAGAGGGAGATCACCTTCCAGCGCGCGCGAGGATGACGCTGAGCTACAGCGCC 373
Qy 443 GCGCCCTTGGCCAGCTGATGCGGCTGATCTACCAACAGGATGGCGCGCTGACCAACCGAG 502
Db 374 GCGCCCTTGGCCAGCTGATGCGGCTGATCTACCAACAGGATGGCGCGCTGACCAACCGAG 433
Qy 503 GTGGCCCTTGGCCCTGGTGTGCGCCACCTGCGAGCAGATGCGCGGACAGCAACCGCAGC 562
Db 434 GTGGCCCTTGGCCCTGGTGTGCGCCACCTGCGAGCAGATGCGCGGACAGCAACCGCAGC 493
Qy 563 CACAGGCGAGTGTGACCAACACACACCCCTGTATCAGGCGAGAGACAGGATGGTGTG 622
Db 494 CACAGGCGAGTGTGACCAACACACACCCCTGTATCAGGCGAGAGACAGGATGGTGTG 553
Qy 623 GCCAGCACACCGCAAGGGCCATGAGCAGATGCGCGCGAGCAGCAGCGCGCGCGAG 682
Db 554 GCCAGCACACCGCAAGGGCCATGAGCAGATGCGCGCGAGCAGCAGCGCGCGCGAG 613
Qy 683 GCCATGGAGGTGGCCAGCGAGCGCGAGGATGTTGTGAGGCGCATGAGGACCATCGGCACC 742
Db 742

Db 614 GCCATGGAGGTGGCCAGCGAGCGCGAGGATGTTGTGAGGCGCATGAGGACCATCGGCACC 673
Qy 743 CACCCAGCAGCAGCGCGCGCTGGAAGAACGACCTGCTGGAGAACCTTGCAGGCGCTACCAG 802
Db 674 CACCCAGCAGCAGCGCGCGCTGGAAGAACGACCTGCTGGAGAACCTTGCAGGCGCTACCAG 733
Qy 803 AAGCGCATGGCGTGCAGATGACGCGCTTCAAGTGAACCTAGT 844
Db 734 AAGCGCATGGCGTGCAGATGACGCGCTTCAAGTGAACCTAGT 775

RESULT 4
US-10-729-830-6
; Sequence 6, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingrid
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; FILE OF INVENTION: Optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 942
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA with increased G/C-content and
; OTHER INFORMATION: stabilisation sequences
; FEATURE:
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
; OTHER INFORMATION: respectively.
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
; OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-6

Query Match 90.3%; Score 762; DB 8; Length 942;
Best Local Similarity 87.9%; Pred. No. 1.8e-170;
Matches 670; Conservative 92; Mismatches 0; Indels 0; Gaps 0;
Qy 83 AGCTGTGACCGAGGTGGAGACCTACGTGTGAGCATCATCCCGAGCGGCCCTGAAG 142
Db 59 AGCCUGUGUACCGAGGUGGAGACCUACGUGUGAGCAUACUCCAGCGGCCCGCCUGAAG 118
Qy 143 GCCGAGATGCCCGAGGCTGGAGAGCTGTTTCGCGCGCAAGAACACCGACCTGGAGTG 202
Db 119 GCCGAGAUCCCGAGGCTGGAGAGCTGTTTCGCGCGCAAGAACACCGACCTGGAGTG 178
Qy 203 CTGATGGATGGCTGAGACAGCGCCCATCTGTAGCCCTTGACCAAGGGCATCTGGGC 262
Db 179 CUGAUGGAGUGGUGAAGACAGCGCCCAUCCUGAGCCCGCCCGCCCGCCUGCGGAG 238
Qy 263 TTCGTGTTACCTTGACCGTCCAGCGCGCGCTGCGAGCGCGCGCTGCGCGCGCTGTCGAG 322
Db 239 UUGUGUUAUCCCGAGCCGUGCCAGCGAGCGCGCGCCUGCGAGCGGCCCGCCUGCGGAG 298
Qy 323 AACGCCCTGAACGGCAACGGCGACCCCAACATGGAACAGGCGCGTGAAGCTGTACAGG 382
Db 299 AACGCCCTGAACGGCAACGGCGACCCCAACATGGAACAGGCGCGGUGAAGCUGUACAGG 358
Qy 383 AAGCTGAGAGGGAGATCACCTTCCAGCGCGCGCAAGAGATGACGCTGAGCTACAGGCGCC 442
Db 359 AAGCUGAAGAGGAGAUACCUUCCAGCGCGCGCAAGAGAGAUACGCGCUGAGCUACAGCGCC 418

[illegible]

RESULT 5
US-10-866-484-9
; Sequence 9, Application US/10866484
; Publication No. US20050013826A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, M.
; APPLICANT: Shneider, A.
; TITLE OF INVENTION: Vaccine Compositions and Methods
; FILE REFERENCE: 25955-003CIP
; CURRENT APPLICATION NUMBER: US/10/866,484
; CURRENT FILING DATE: 2004-06-11
; PRIOR APPLICATION NUMBER: 60/435,500
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 10/741,466
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 986
; TYPE: DNA
; ORGANISM: Influenza A virus
US-10-866-484-9

Query Match	58.5%;	Score 494;	DB 8;	Length 986;
Best Local Similarity	78.2%;	Prod. No. 3.7e-107;		
Matches 593;	Conservative	0; Mismatches 165;	Indels	0; Gaps 0
Qy	83	AGCCTGCTGACCGAGTGGAGACCTACGTGCTGTGAGCATCATCCACGCGGCCCCCTGAAG	142	
Db	4	AGTCTTCTAACCGAGTGCAGACGTACGTTCTCTATCGTCCGTCAGGCCCCCTCAA	63	
Qy	143	GCCGAGATGCCCCGAGGCTGGAGGACGTGTTCGCCGCGAAGAACACCGACCTGGAGGTG	202	
Db	64	GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGTCTGGGAAGAACCCGATCTCGAGGCA	123	
Qy	203	CTGATGGAGTGGCTCAAGACACGAGGCCATCTCTGAGGCCCTCTACCAAGGGCATCTCTGGGC	262	
Db	124	CTCATGGAATGGCTAAGACAGACCAATCTGTCACTCTGACTAAGGGATTTTAGGA	183	
Qy	263	TTGCTGTTTCA CCTGACCGTGCACGAGCGGGCTCGAGGGCCGCGCTTCGTGTCAG	322	
Db	184	TTTGTGTTTCA CGCTCACCGTGCACGAGTGCAGGAGACTCGACGCTAGACGCTTTGTGCCAG	243	
Qy	323	AACGCCCTTGAA CGGGCAACGGCGCACCCCAACAAACATGCAACGAGCCCGTGAAGCTGTACAGG	382	

[illegible]

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RESULT 6
US-10-729-830-5
; Sequence 5, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCI/CIP
; CURRENT APPLICATION NUMBER: US/10/729.830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 942
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA with stabilisation sequences
; FEATURE:
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
; OTHER INFORMATION: respectively.
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
; OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
; US-10-729-830-5

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Query Match 57.7%; Score 486.8; DB 8; Length 942;
Best Local Similarity 65.4%; Pred. No. 1.8e-105;
Matches 498; Conservative 92; Mismatches 172; Indels 0; Gaps 0

;
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Influenza virus
; US-10-177-390-31

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Query Match      57.0%; Score 481.2; DB 6; Length 1027;
Best Local Similarity 77.2%; Pred. No. 3.9e-104;
Matches 585; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

QY 83 AGCCTGCTGACCGAGGTGGAGACCTAGTGTCTGAGCATCATCCCGAGCGGCCCTCTGAAG 142
DB 29 AGTCTTTAAACCGAGGTGGAACGTAAGTCTCTCTATCATCCCGTCAGGCGCCCTCAAA 88

QY 143 GCCGAGATCGCCAGAGGCTGGAGGACGTGTTCGCGCAAGAACACCGACCTGGAGGTG 202
DB 89 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGACGGAAGAACACCGATCTTGAGGTT 148

QY 203 CTGATGAGTGGCTGAAGACAGAGCCCATCTCTGAGCCCTTGACCAAGGGCATCTCGGC 262
DB 149 CTCATGGAATGGCTAAAGACAGACCAATCTCTGACCTCTGACTAAGGGGATTTTAGGA 208

QY 263 TTGCTGTTACCTGACCGTCCAGAGGCGCGCTGACGCGCCCGCTTCTGTCGAG 322
DB 209 TTTGTGTTACGCTCACCGTCCAGTGAGGCGAGCATGACGCTGAGCGCTTTGTCAA 268

QY 323 AACGCCCTGAACGGCAACGGCGACCCCAACAACTGGAACAGGCGCTGAAGCTGTACAGG 382
DB 269 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAGCAGTTAAACTGTATAGG 328

QY 383 AAGCTGAAGAGGAGATCACCTTCAAGCGCCCAAGGAGATGACGCTGAGTACAGGCC 442
DB 329 AAGCTCAAGAGGAGATTAACATTTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 388

QY 443 GGCGCCCTGGCAGCTGATGGGCTGTGATCTACAAAGAGTGGCGCGCTGACCAACCGAG 502
DB 389 GGTGCACTTGCCAGTTGTATGGGCTCTATATACAAAGGATGGGGCTGTGACCACTGAA 448

QY 503 GTGCGCTTGGCCTGTGTCGCGCACTGCGCAGCAGATCGCGCAGACGCAAGCAGCGCAGC 562
DB 449 GTGGCAATTTGGCCTGTGTCGCAACCAACCCACTAATCAGACATGAGAACAGAAATGGTTTA 568

QY 623 GCCAGCACACCGCCAGGCCATGGAGCAGATGGCGGCGCAGCAGCGCGCCGAG 682
DB 569 GCCAGCACTACAGCTAAGGCTATGGAGCAATATGGCTGTGATCGAGTGAAGCAGCAGAG 628

QY 683 GCCATGAGGTGGCGCAGCGCCAGCGCAGTGTGTCAGGCGCATGAGGACCATCGGCACC 742
DB 629 GCCATGAGGTGTCTAGTCAGGCTAGGCAATATGGTGTCAAGCATGAGAACCATTTGGGACT 688

QY 743 CACCCAGCAGCAGCGCGCGCTGAGAACACCTGCTGGAGAACCTTGAGGACCTTACCAG 802
DB 689 CATCTAGCTCCAGTGTGCTGTGAAATAATGATCTCTTTGAAATAATTTGAGGACCTATCAG 748

QY 803 AAGCGCATGGCGGTGCAGATCAGCGCTTCAAGTGAAC 840
DB 749 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 786
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RESULT 9
US-10-855-875-5
; Sequence 5, Application US/10855875
; Publication No. US2005000349A1

;
; GENERAL INFORMATION:
; APPLICANT: Kawaoka, Yoshihiro
; TITLE OF INVENTION: High Titer Recombinant Influenza Viruses for Vaccines and Gene
; FILE REFERENCE: 800.038US1
; CURRENT APPLICATION NUMBER: US/10/855,875
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: US 60/473,798
; PRIOR FILING DATE: 2003-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Influenza virus
; US-10-855-875-5

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Query Match      56.6%; Score 478; DB 8; Length 1027;
Best Local Similarity 76.9%; Pred. No. 2.2e-103;
Matches 583; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

QY 83 AGCCTGCTGACCGAGGTGGAGACCTAGTGTCTGAGCATCATCCCGAGCGGCCCTCTGAAG 142
DB 29 AGTCTTTAAACCGAGGTGGAACGTAAGTCTCTCTATCATCCCGTCAGGCGCCCTCAAA 88

QY 143 GCCGAGATCGCCAGAGGCTGGAGGACGTGTTCGCGCAAGAACACCGACCTGGAGGTG 202
DB 89 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGACGGAAGAACACCGATCTTGAGGTT 148

QY 203 CTGATGAGTGGCTGAAGACAGCGCCCATCTCTGAGCGCCCTTGACCAAGGGCATCTCGGC 262
DB 149 CTCATGGAATGGCTAAAGACAGACCAATCTCTGACCTCTGACTAAGGGGATTTTAGGA 208

QY 263 TTGCTGTTACCTGACCGTCCAGAGGCGCGCTGACGCGCCCGCTTCTGTCGAG 322
DB 209 TTTGTGTTACGCTCACCGTCCAGTGAGCGGAGCTGACGCGCTTTGTCAA 268

QY 323 AAGGCCCTGAACGGCAACGGCGACCCCAACAACTGGAACAGGCGCTGAAGCTGTACAGG 382
DB 269 AATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAGCAGTTAAACTGTATAGG 328

QY 383 AAGCTGAAGAGGAGATCACCTTTCAGCGCGCCAAAGAGATGACGCTGAGCTACAGCGCC 442
DB 329 AAGCTCAAGAGGAGATTAACATTTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCTGCT 388

QY 443 GGCGCCCTGGCAGCTGATGGGCTGTGATCTCAACAGGATGGCGCGCTGACCAACCGAG 502
DB 389 GGTGCACTTGCCAGTTGTATGGGCTCTATATACAAAGGATGGGGCTGTGACCACTGAA 448

QY 503 GTGCGCTTGGCCTGTGTCGCGCACCTGCGAGCAGATCGCGCAGCAGCGCAGCGCAGC 562
DB 449 GTGGCAATTTGGCCTGTGTCGCAACCTGTGAACAGATTTGCTGACTCCAGCATCGGTCT 508

QY 563 CACAGGCAGATGTGTGACCAACCAACCCCTGATCAGGCAAGCAGCAAGATGGTGTG 622
DB 509 CATAGGCANATGGTGACAACAACCAATCCACTAATCAGACATGAGAACAGAAATGGTTTA 568

QY 623 GCCAGCACACCGCCAGGCCATGGAGCAGATGGCGGCGCAGCAGCGCGCCGAG 682
DB 569 GCCAGCACTACAGCTAAGGCTATGGAGCAATATGGCTGTGATCGAGTGAAGCAGCAGAG 628

QY 683 GCCATGAGGTGGCGCAGCGCCAGCGCAGTGTGTCAGGCGCATGAGGACCATCGGCACC 742
DB 629 GCCATGAGGTGTCTAGTCAGGCTAGGCAATATGGTGTCAAGCATGAGAACCATTTGGGACT 688

QY 743 CACCCAGCAGCAGCGCGCGCTGAGAACACCTGCTGGAGAACCTTGAGGACCTTACCAG 802
DB 689 CATCTAGCTCCAGTGTGCTGTGAAATAATGATCTCTTTGAAATAATTTGAGGACCTATCAG 748

QY 803 AAGCGCATGGCGGTGCAGATGCAACGGTTCAAGTGAAC 840
DB 749 AAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATC 786
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RESULT 10
US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-065-133A-1

Query Match 56.6%; Score 477.6; DB 6; Length 1023;
Best Local Similarity 76.8%; Pred. No. 2.8e-103;
Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;

Qy	83	AGCCTGCTGACCGAGTGGAGACCTACGCTGTGAGCATCATCCCGAGCGGCCCTCTGAAG	142
Db	28	AGTCTTCTGACCGAGTTCGAACGTACGTTCTCTATCGTACCATCAGGCCCTCAA	87
Qy	143	GCCGAGATGCGCCAGAGCTGGAGACGTTGTCGCCGCAAGAACACCGACTGGAGTG	202
Db	88	GCCGAGATGCGCCAGAGCTTGAAGATGTTCTTGCAGGGAAGAACACCGATCTTGAGCA	147
Qy	203	CTGATGGAGTGGCTGAACACGAGCCCATCTGAGCCCTGACGCGCGCGCTTCGTGCAG	262
Db	148	CTCATGGAATGGCTAAAGACAAGACCAATCTCTGACTGACTAAAGGATTTTGA	207
Qy	263	TTGCTGTTTACCGCTGACCTGACCGCGCGCGCTGACGCGCGCGCTTCGTGCAG	322
Db	208	TTGCTGTTTACCGCTGACCTGACCGCGCGCGCTGACGCGCGCGCTTCGTGCAG	267
Qy	323	AACGCCCTTGAACCGGCAACCGCCCAACCAATGGAACAAGCGCGTGAAGCTGTACAGG	382
Db	268	AATGCCCTTAGTGGAAACCGAGATCCAAACCAACATGGAACAGACGAGTAAAACTGTACAGG	327
Qy	383	AAGCTGAGAGGAGATCACCTTCCACGCGCGCGCGCGCTGACGCTGAGTACAGCGCC	442
Db	328	AAGCTTAAAGAGAAATTAACATTCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT	387
Qy	443	GCGCGCTTGGCGAGCTGATGCGGCTGATCTACACAGATGGCGCGCGCTGACCAACCGAG	502
Db	388	GGTGACTAGCGAGCTGATGGGACTCATATACAGAAATGGGAACTGTGACAAACCGAA	447
Qy	503	GTGGCTTTCGCTGGTGTGCGCCACTTCGAGCAGAGATTCGCGCAGCAGCAGCGCAGC	562
Db	448	GTGGCATTTGGCTGGTATGCGCCACATGTGAACAGATCGCTGATTCACCGCATCGATCT	507
Qy	563	CACAGGAGATGGTGACCAACCAACCCCTGTATCAGGACAGGAGAACAGAGATGGTGTG	622
Db	508	CACAGGAGATGGTGACCAACCAACCCCTGTATCAGGACAGGAGAACAGAGATGGTATTA	567
Qy	623	GCCAGCACCGCCCAAGGCCATGGAGCAGATGGCGCGCGCGCGCGCGCGCGCGCGCG	682

Db	568	GCCAGTACCACCGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTGAGCAGGACGAG	627
Qy	683	GCCATGAGGTGGCCAGCCAGCCAGCAGATGGTGCAGGCCCATGAGGACCATCGGCACC	742
Db	628	GCCATGAGGTGCTAGTAAGGCTAGGCAGATGGTRCAGGCAATGAGAACCATTTGGGACC	687
Qy	743	CACCCAGCAGCAGCGCGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCGCTACACAG	802
Db	688	CACCTAGCTCCAGTGCCGGTTTGAAGATGATCTCTTGAATTTTGCAGGCGCTACACAG	747
Qy	803	AAGCGCATGGCGTGCAGATGCAGCGCTTCAAGTGAAC	840
Db	748	AAACGGATGGAGTGCAATGCAGCGATTCAGGTGATC	785

RESULT 11
US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (663)..(663)
; OTHER INFORMATION: At nucleotide 663, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-434-811A-1

Query Match 56.6%; Score 477.6; DB 7; Length 1023;
Best Local Similarity 76.8%; Pred. No. 2.8e-103;
Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;

Qy	83	AGCCTGCTGACCGAGTGGAGACCTACGCTGTGAGCATCATCCCGAGCGGCCCTCTGAAG	142
Db	28	AGTCTTCTGACCGAGTTCGAACGTACGTTCTCTATCGTACCATCAGGCCCTCAA	87
Qy	143	GCCGAGATGCGCCAGAGCTGGAGACGTTGTCGCCGCAAGAACACCGACTGGAGTG	202
Db	88	GCCGAGATGCGCCAGAGACTTGAAGATGTTCTTGCAGGGAAGAACACCGATCTTGAGCA	147
Qy	203	CTGATGGAGTGGCTGAACACGAGCCCATCTGAGCCCTGACGCGCGCGCTTCGTGCAG	262
Db	148	CTCATGGAATGGCTAAAGACAAGACCAATCTCTGACTGACTAAAGGATTTTGA	207
Qy	263	TTGCTGTTTACCGCTGACCTGACCGCGCGCGCTGACGCGCGCGCTTCGTGCAG	322
Db	208	TTGCTGTTTACCGCTGACCTGACCGCGCGCGCTGACGCGCGCGCTTCGTGCAG	267
Qy	323	AACGCCCTTGAACCGGCAACCGCCCAACCAATGGAACAAGCGCGTGAAGCTGTACAGG	382
Db	268	AATGCCCTTAGTGGAAACCGAGATCCAAACCAACATGGAACAGACGAGTAAAACTGTACAGG	327
Qy	383	AAGCTGAGAGGAGATCACCTTCCACGCGCGCGCGCGCTGACGCTGAGTACAGCGCC	442
Db	328	AAGCTTAAAGAGAAATTAACATTCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT	387
Qy	443	GCGCGCTTGGCGAGCTGATGCGGCTGATCTACACAGATGGCGCGCGCTGACCAACCGAG	502
Db	388	GGTGACTAGCGAGCTGATGGGACTCATATACAGAAATGGGAACTGTGACAAACCGAA	447
Qy	503	GTGGCTTTCGCTGGTGTGCGCCACTTCGAGCAGAGATTCGCGCAGCAGCAGCGCAGC	562
Db	448	GTGGCATTTGGCTGGTATGCGCCACATGTGAACAGATCGCTGATTCACCGCATCGATCT	507
Qy	563	CACAGGAGATGGTGACCAACCAACCCCTGTATCAGGACAGGAGAACAGAGATGGTGTG	622
Db	508	CACAGGAGATGGTGACCAACCAACCCCTGTATCAGGACAGGAGAACAGAGATGGTATTA	567
Qy	623	GCCAGCACCGCCCAAGGCCATGGAGCAGATGGCGCGCGCGCGCGCGCGCGCGCGCG	682

Qy 383 AAGCTGAAGAGGGAGATCACTTCCACGGGCGCCAAAGAGATCAGCCCTGAGCTACAGCGCC 442
Db 328 AAGCTTAAAGAGAAATAACATTCATGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387
Qy 443 GGCGCCCTGGCCAGCTGCATGGGCTGATCTACACAGGATGGGCGCGTGACCAACGAG 502
Db 388 GGTGCATAGCAGCTGCATGGGACTCATATACAAACAGAAATGGGAACTGTGACAACCGAA 447
Qy 503 GTGGCCCTTGGCCCTGGTGGCCACCTCGAGCAGATCGCCGACAGCCAGCAGCCGAGC 562
Db 448 GTGGCAATTTGGCCCTGGTATGGCCACATGTGAACAGATCGTGTATCCAGCATCGATCT 507
Qy 563 CACAGGAGATGGTGACACCAACCAACCCCTGTATCAGGCAAGAGAAACAGGATGGTGTG 622
Db 508 CACAGGAGATGGTGACAAACCAACCAACCCATTAATCAGACATGAAACAGAAATGGTATTA 567
Qy 623 GCCAGCACCCGCAAGGCCATCGAGCAGATGGCGGCAGCAGCAGCAGCGCCGAG 682
Db 568 GCCAGTACCAAGCGCTAAAGCCATGGAGCAGATGGCAGGGTTCGATGAGCAGGCGCAGAG 627
Qy 683 GCCATGAGGTGGCGAGCAGCGCCAGGCGAGATGGTGAGGCGCATGAGGACCATCGGCACC 742
Db 628 GCCATGAGGTGGTGTAGTAAAGCTAGGCGATGGCGAGATGGTGCAGCAATGAGAACCATTTGGGACC 687
Qy 743 CACCCAGCAGCAGCGCGGCTGAAAGAACGACCTGTCTGGAGAACCTGCGAGGCGCTACAG 802
Db 688 CACCCTAGCTCAGTGGCGGTTTGAAGATGATCTCTCTTGAATAATTTGCGAGGCGCTACAG 747
Qy 803 AAGCGCATGGCGTGCAGATCGAGGCTTCAAGTGAAC 840
Db 748 AAACGGATGGGATGCAAAATCGACGATTTCAAGTGATC 785

RESULT 12

US-10-734-373-1
; Sequence 1, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, xaa = Val
US-10-734-373-1

Query Match 56.6%; Score 477.6; DB 7; Length 1023;
Best Local Similarity 76.8%; Pred. No. 2.8e-103;
Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;
Qy 83 AGCCTGCTGACCGAGGTGGAGACCTACGCTGTGACATCATCCCCAGCGGCCCTGAAG 142
Db 28 AGTCTTCTGACCGAGGTGGAACGTTACCTTCTCTAATGTTACATGAGCGGCCCTCAAA 87

Qy 143 GCCAGATGCCCGACAGGCTGGAGAGCTGTTCGCCGGCAGAAACACCCGACCTGGAGGTG 202
Db 88 GCCAGATGCCCGCAGAGACTTGAAGATGTCTTTGTCAGGGGAAGAACACCCGATCTTGAGGCA 147
Qy 203 CTGATGGAGTGGCTGAAGACACGAGCCCATCTCAGAGCCCTGACCAAGGGGCATCTTGGGC 262
Db 148 CTATGGAATGGCTAAAGACAGACCAATCTCTGCTACCTTGACTAAAGGATTTTAGGA 207
Qy 263 TTCTGTGTTCACTCCCTGACCGTCCAGCAGCGCGCTTCAGCGCCCGCCCTGCTGTGTCAG 322
Db 208 TTCTGTTTCACTCCCTGACCGTCCAGTGGAGGAGTGCAGCGTAGACGCTTTGTCAA 267
Qy 323 AAGCCCTTGAACGGCAACGGCGACCCCAACACATGACAGGCGCTGAGCTGTACAGG 382
Db 268 AATGCCCTTGTAGTGGAAACGGAGATCCAAACCAACATGACAGACGAGCTTAAACCTGTACAGG 327
Qy 383 AAGCTGAAGAGGAGATCACTTCCAGCGCGCCCAAGAGATCAGCCTGAGCTACAGCGCC 442
Db 328 AAGCTTAAAGAGAAATAACATTTCCATGGGGCAAGAGGTGGCACTCAGCTATTCCACT 387
Qy 443 GGCGCCCTGGCCAGCTGCATGGGCTGATCTCAACACAGATGGCGCGCTGACCAACCGAG 502
Db 388 GGTGCATAGCAGCTGCATGGGACTCATATACACAGAAATGGGAACTGTGACAACCGAA 447
Qy 503 GTGGCCCTTGGCCCTGTGTGGCCACCTGCGGACAGATCGCCGACAGCAGCAGCCGAGC 562
Db 448 GTGGCATTTGGCCCTGTGTGGCCACATGTGAAACAGATCGCTGATTTCCGAGCATCGATCT 507
Qy 563 CACAGCAGATGTGTGACCAACCAACCCCTCATCAGGCACGAGAACAGATGGTGTCTG 622
Db 508 CACAGCAGATGTGTGACAAACCAACCCCTTAATCAGACATGAAACAGAAATGGTATTA 567
Qy 623 GCCAGCACCAACCGCCCAAGGCCATGAGCAGATGGCGGCAGCAGCAGCAGCGCGCGAG 682
Db 568 GCCAGTACCAACCGCTAAAGCCATGGAGCAGATGGCAGGGTTCGATGAGCAGGCGCAGAG 627
Qy 683 GCCATGAGGTGGCGAGCGCAGCGCAGCAGATGGTGAGGCCCATGAGGACCATCGGCACC 742
Db 628 GCCATGAGGTGGTGTAGTAAAGCTAGGCTAGGCGATGGTTCAGGCNAATGAGAACCATTTGGGACC 687
Qy 743 CACCCAGCAGCAGCGCGGCTGAAAGACGACCTGTCTGGAGAACCTGCGAGGCGCTACAG 802
Db 688 CACCCTAGCTCAGTGGCGGTTTGAAGATGATCTCTTGAATAATTTGCGAGGCGCTACAG 747
Qy 803 AAGCGCATGGCGTGCAGATGAGCGCTTCAAGTGAAC 840
Db 748 AAACGGATGGGATGCAAAATGCAGCGATTTCAAGTGATC 785

RESULT 13

US-10-872-014-1
; Sequence 1, Application US/10872014
; Publication No. US20040234553A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/872,014
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/434,811
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 09/762,861
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1


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/ LENGTH: 1023
/ TYPE: DNA
/ ORGANISM: Equine influenza virus H3N8
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (25)..(780)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (663)..(663)
/ OTHER INFORMATION: At nucleotide 663, r = a or g
/ OTHER INFORMATION: At amino acid residue 213, xaa = Val
US-10-872-014-1

Query Match          56.6%; Score 477.6; DB 8; Length 1023;
Best Local Similarity 76.8%; Pred. No. 2.8e-103;
Matches 582; Conservative 1; Mismatches 175; Indels 0; Gaps 0;

QY 83 AGCTGCTGACCGAGTGGAGACCTACGTGCTGAGCATCATCCCGAGGCGCCCTGGAAG 142
Db 28 AGTCTTCTGACCGAGTGGAAAGTACGTTCCTCTATCGTACCATCAGGCCCTCAA 87

QY 143 GCCGAGATGCCGAGAGCTGGAGACGTGTTGCGCGGCAAGAACACCGACTGTGAGGTG 202
Db 88 GCCGAGATGCCGAGAGCTTGAAGATGTCTTTGCGGGAAGAACACCGACTTTGAGGCA 147

QY 203 CTGATGAGTGGCTGAAGACAGGCCCATCTCTGAGCCCTTGACCAAGGGCATCTGGGC 262
Db 148 CTCATGGAATGGCTAAAGACAGCAATCTCTGACCTCTGACTAAAGGATTTTGA 207

QY 263 TTGCTGTTTCACTTGCACCGTGCACGAGCGCGCTTGCAGCGCGCTTGTGCGAG 322
Db 208 TTGCTATTTACGCTCACCGTGCACGAGTGCAGGAGTGCAGCGTGTGTCACAA 267

QY 323 AACGCCCTGAACGGCAACGGGACCCCAACATGGAAGGACCGTGAACCTGTACAGG 382
Db 268 AATGCCCTTAGTGGAAACGGAGATCAAAACAACTGGAACAGAGCAAGTAAACTGTACAGG 327

QY 383 AAGCTGAAGAGGAGATCACCTTCCACGCGCCGAAGGAGATCAGCTGAGCTACAGCGCC 442
Db 328 AAGCTTAAAGAGAAATAACATTTCCATGGGGCAAAAGAGGTGGCACTACGCTATTCCACT 387

QY 443 GGCGCTTGGCGAGCTGATGGGCTGATCTAACAAGATGGGCGCGTGCACCAACCGAG 502
Db 388 GGTGCACTAGCCAGCTGATGGGACTATATACACAGATGGGNACTGTGCAACCGAA 447

QY 503 GTGGCTTTGGGCTGTGTGCGCCACCTTGCAGAGCAGATCGCCGACAGCCAGCCGACG 562
Db 448 GTGGCATTTGGCTGTGTGCGCCACATGTGAACAGATCGCTGATTTCCAGCATCGATCT 507

QY 563 CACAGGAGATGGTGACCAACCAACCCCTGTGATCAGGCAAGAGATGGTGTG 622
Db 508 CACAGGAGATGGTGACCAACCAACCCCTTAATCAGACATGAACAGAAATGGTATTA 567

QY 623 GCCAGCACACCGCCCAAGGCTTGAAGCAGATGGCGCGCAGCAGCAGCGCCCGCGAG 682
Db 568 GCCAGTACCAACCGCTTAAGCCATGGAGCAGATGGCAGGCTCGAGTGCAGCAGCAGAG 627

QY 683 GCCATGAGGTGGCCAGCCAGCCAGGAGCAGATGGTGCAGGCGATGAGGACCATCGGCACC 742
Db 628 GCCATGAGGTGGCTAGTAAAGCTAGGAGCAGATGGTTCAGGCAATGAGAACCATTTGGGACC 687

QY 743 CACCCAGCAGCAGCGCGCTGAGAACCCCTGTGAGAACCTGTGAGAACCTGTGAGGCTTACCAG 802
Db 688 CACCCTAGCTCCAGTGGCGGTTTGAAGATGATCTCTCTTGAATAATTTGAGGCGCTTACCAG 747

QY 803 AAGCGCATGGGCGTGCAGATCAGCGCTTCAAGTGAAC 840
Db 748 AAACGGATGGGAGTGCAAATGCAGCGATTCAGTGATC 785

RESULT 14
US-10-371-525-13
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/ Sequence 13, Application US/10371525
/ Publication No. US20030203869A1
/ GENERAL INFORMATION:
/ APPLICANT: Fikes, John D.
/ APPLICANT: Hermanson, Gary G.
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Ishioka, Glenn Y.
/ APPLICANT: Livingston, Brian
/ APPLICANT: Cheenut, Robert W.
/ APPLICANT: Epimmune Inc.
/ TITLE OF INVENTION: Expression Vectors for Stimulating an
/ TITLE OF INVENTION: Immune Response and Methods of Using the Same
/ FILE REFERENCE: 39963-20022.01
/ CURRENT APPLICATION NUMBER: US/10/371,525
/ PRIOR FILING DATE: 2003-02-21
/ PRIOR APPLICATION NUMBER: US 09/311,784
/ PRIOR FILING DATE: 1999-05-13
/ PRIOR APPLICATION NUMBER: US 60/085,751
/ PRIOR FILING DATE: 1998-05-15
/ NUMBER OF SEQ ID NOS: 463
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 13
/ LENGTH: 816
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
/ OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of
/ OTHER INFORMATION: Influenza matrix protein gene
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (16)...(816)
/ OTHER INFORMATION: PADRE-Influenza matrix
US-10-371-525-13

Query Match          56.6%; Score 477.4; DB 6; Length 816;
Best Local Similarity 75.6%; Pred. No. 3.1e-103;
Matches 592; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

QY 56 GCCCTGCGCTGACCCAGACCTGGGCTAGCTGCTGACCGAGGTGGAGACCTAGCTGCTG 115
Db 34 GCCTGGACCTCGAAGGCTGCGCTATGAGTCTTCTAACCGAGGTGCGAAACGTACGTTCTC 93

QY 116 AGCATCATCCCGAGCGCCCTCGAAGCGAGATCCCGCAGAGGCTGGAGAGCGTGTTC 175
Db 94 TCTATCATCCATCAGCGCCCTCAAAGCCGAGATCCGCGAGACCTTGAGATGTTTTT 153

QY 176 GCGCGCAAGAACACCGACCTGGAGGTGCTGATGGAGTGGCTGAAGACAGGCCCATCTG 235
Db 154 GCAGGGAAGAACACAGATCTTGAGGCTCTCATGGAATGGCTTAAAGACAGACCAATCCTG 213

QY 236 AGCCCCCTGACCAAGGCGATCCTGGGCTTCTGTTTCACTGACCGTGGCCAGCGAGCGC 295
Db 214 TCACCTCTGACTAAGGGAATTTTGGGTTTGTGTTACGCTCACCGTGGCCAGTGAGCGGA 273

QY 296 GGCCTGAGCGCGCGCTTCTGTCAGAACGCGCTGAAACGCGCAACGCGACGCCCAACAC 355
Db 274 GGACTGAGCGTAGACGATTTGTCAAAATGCCCCATTAATGGGAATGGAGACCCCAACAC 333

QY 356 ATGACAAAGCCCGTGAAGCTGTACAGGAAGCTGAAGAGGAGATCACTTTCCAGCGGCC 415
Db 334 ATGACAGGCGCAGTTAACTATATACAAAGCTGAAGAGGGAATGACATTCATCGAGCA 393

QY 416 AAGGAGATCAGCTGAGCTACAGCGCGCGCGCTGCGCAGCTGCATGGGCGCTGATCTAC 475
Db 394 AAGGAAGTTGCACCTCAGTTTACTCAACTGGTGGCGCTGCGCTGCGATGGGTCTCATATAC 453

QY 476 AACAGGATGGCGCGCTGACACCGAGGTGGCTTTCGGCTGGTGTGCGCACCTGCGAG 535
Db 454 AACCGATGGGAACAGTGAACCAAGAGTGGCTTTCGGCTGTATGTGCCACTTGTGTGAG 513

QY 536 CAGATCGCCGACAGCCAGCCGAGCTACAGGAGATGGTGAACACCAACCCCTG 595
Db 513 CAGATCGCCGACAGCCAGCCGAGCTACAGGAGATGGTGAACACCAACCCCTG 595
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Db 514 CAGATTGCTGATGCCCAACATCGGTCCCAAGGCGATGGGACTACCAACCAACCCACTA 573
Qy 596 ATCAGGCACGAGAACAGGATGGTGTCTGGCCAGCACACCGCCCAAGGCCATGGAGCAGATG 655
Db 574 ATCAGGCATGAGAACAGATGGTACTAGCCAGCACTACGGCTAAGGCCATGGAGCAATG 633
Qy 656 GCCGGCAGCAGCAGCAGCGCCCGCAGGCCATGAGAGTGGCCAGCCAGGCCAGGCAGATG 715
Db 634 GCTGGATCAAGTGAGCAGCGCAGCAGAGGCCATGGAAGTCGCAAGTCAGGCTAGACAAATG 693
Qy 716 GTGCAGGCCATGAGGACCATCGGCACACCCAGCAGCAGCGCGCCCTGAAGAAGCAC 775
Db 694 GTGCAGGCAATGAGGACAAATTGGGACTCACCCCTAGCTCCAGTGCAGGTCTAAAGATGAT 753
Qy 776 CTGCTGGAGAACCTCGAGGCCCTACCAAGAGCGCATGGGCGTGCAGATGCAGCGCTTCAAG 835
Db 754 CTTATTGAAATTTGCGAGGCTTACCAGAAACGGATGGGGTGCAGATGCAGCGATTTCAAG 813
Qy 836 TGA 838
Db 814 TGA 816

RESULT 15

US-10-371-069-13
; Sequence 13, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Cheenut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
; OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of
; OTHER INFORMATION: Influenza matrix protein gene
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16)...(816)
; OTHER INFORMATION: PADRE-Influenza matrix
; US-10-371-069-13

Query Match 56.6%; Score 477.4; DB 6; Length 816;
Best Local Similarity 75.6%; Pred. No. 3.1e-103;
Matches 592; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

Qy 56 GCCCTGGCCCTGACCCAGACCTGGGCTAGCTGTGTCGAGGTGGAGACCTACGTGCTG 115
Db 34 GCCTGGACCTGGAAGGGCTGCCGCTATGAGTCTTTAAACCGAGGTGGAACGTACGTTCTC 93
Qy 116 AGCATCATCCCGAGCGCCCTCTGAAGGCCGAGATCGCCAGAGCGCTGGAGGACGTGTC 175
Db 94 TCTATCATCCCATCAGGCGCCCTCAAGCCCGAGATCGCGCAGAGACTTGAGAGTGTITT 153

Qy 176 GCCGCAAGAACACCCACCTGGAGGTGCTGATGGAGTGGCTGAAGACCCAGGCCACCTCTG 235
Db 154 GCAGGGAAGAACACAGATCTTGAGGCTCTCATGGAATGGCTAAAGACACAGACCAATCTCTG 213
Qy 236 AGCCCTCTGACCAAGGGCATCTTGGGCTTCGTGTTTCACTGACCGTGGCCAGCGAGCGC 295
Db 214 TCACCTCTGACTAAGGGAATTTTAGGGTTTGTGTTTCACTGACCGTTCACCGTGGCCAGTGAGCGA 273
Qy 296 GGCTCTCAGCGCCCGCCGCTTCGTGCAAGACGCCCTGAAACGGCAACGGCGGACCCCAACAC 355
Db 274 GGACTCGAGCTAGACGATTTGTCCAAATGCCCCTAAATGGGAATGGAGACCCCAACAC 333
Qy 356 ATGACCAAGGCCCTGAGCTGTACAGGAGCTGAAGAGGGAGATCACTTCCACGGCGCC 415
Db 334 ATGGAAGGGGCACTTAAACCTATACAAGAGCTGAAGAGGGAATGACATTTCCATGGAGCA 393
Qy 416 AAGGAGATCAGCTGAGCTACAGCGCGCGCCCTGGCCAGCTGCATGGGCTCTGATCTAC 475
Db 394 AAGGAATGGCACTCAGTTACTCAACTGGTGGCTTGGCAGTTGCATGGGTCTCATATAC 453
Qy 476 AACAGGATGGCGCCCGTGAACACCGAGGTGGCTTCGGCCCTGTGTGGCGCCACCTGGCAG 535
Db 454 AACCGGATGGGAACAGTGACCAAGAGTGGCTCTTGGCCTAGTATGTGCTTGTGAG 513
Qy 536 CAGATCGCCGACAGCCAGCACCGCCAGCAGGAGATGGTGACCCACCAACCCCTG 595
Db 514 CAGATTGCTGATGCCCAACATCGGTCCACAGGAGATGGCGACTACCAACCAACCCACTA 573
Qy 596 ATCAGGCACGAGAACAGGATGGTGTGGCCAGCACCAACCGCCCAAGGCCATGGAGCAGATG 655
Db 574 ATCAGGCATGAGAACAGATGGTACTAGCCAGCACTACGGCTAAGGCCATGGAGCAATG 633
Qy 656 GCCCGCAGCAGCAGCAGCGCCCGCAGGCCATGAGAGTGGCCAGCCAGGCCAGGCAGATG 715
Db 634 GCTGGATCAAGTGAGCAGGCGCAGCAGAGGCCATGGAAGTCGAAAGTCAGGCTAGACAAATG 693
Qy 716 GTGCAGGCCATGAGGACCATCGGCACCCAGCAGCAGCGCCGCTGGAAGACGAC 775
Db 694 GTGCAGGCAATGAGGACCAATTTGGGACTCACCTAGCTCCAGTGCAGGTCTTAAAGATGAT 753
Qy 776 CTGCTGGAGAACCTGCAGGCTTACCAGAGCGCATGGGCGTGCAGATGCAGCGCTTCAAG 835
Db 754 CTTATTGAAATTTGCAAGGCTTACCAGAAACGGATGGGGTGCAGATGCAGCGATTTCAAG 813
Qy 836 TGA 838
Db 814 TGA 816

Search completed: March 21, 2006, 13:38:05
Job time : 830.608 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2006, 23:50:55 ; Search time 383.576 Seconds
(without alignments)
5130.555 Million cell updates/sec

Title: US-10-729-830-4
Perfect score: 844
Sequence: 1 agatctaaagatgccgtca.....agcgttcaagtgaactagt 844

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues
Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:
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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB_seq.*
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4: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB_seq.*
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7: /cgn2_6/ptodata/2/pubpna/US12_NEW_PUB_seq.*
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9: /cgn2_6/ptodata/2/pubpna/US14_NEW_PUB_seq.*
10: /cgn2_6/ptodata/2/pubpna/US15_NEW_PUB_seq.*
11: /cgn2_6/ptodata/2/pubpna/US16_NEW_PUB_seq.*
12: /cgn2_6/ptodata/2/pubpna/US17_NEW_PUB_seq.*
13: /cgn2_6/ptodata/2/pubpna/US18_NEW_PUB_seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	730.6	86.6	756	12	US-11-131-479-27	Sequence 27, Appl
2	686.8	81.4	759	12	US-11-131-479-69	Sequence 69, Appl
3	686.8	81.4	1050	12	US-11-131-479-59	Sequence 59, Appl
4	665.2	78.8	982	12	US-11-131-479-61	Sequence 61, Appl
5	664.8	78.8	759	12	US-11-131-479-79	Sequence 79, Appl
6	594.6	70.5	756	12	US-11-131-479-28	Sequence 28, Appl
7	488	57.8	756	12	US-11-131-479-26	Sequence 26, Appl
8	476.4	56.4	1027	12	US-11-131-479-3	Sequence 3, Appl
9	473	56.0	1305	12	US-11-131-479-45	Sequence 45, Appl
10	460.4	54.5	987	12	US-11-155-478A-131	Sequence 131, Appl
11	454	53.8	982	12	US-11-131-479-60	Sequence 60, Appl
12	454	53.8	4822	12	US-11-131-479-95	Sequence 95, Appl
13	454	53.8	5161	12	US-11-131-479-101	Sequence 101, Appl
14	454	53.8	5398	12	US-11-131-479-91	Sequence 91, Appl
15	454	53.8	7798	12	US-11-131-479-97	Sequence 97, Appl
16	454	53.8	7798	12	US-11-131-479-98	Sequence 98, Appl
17	454	53.8	7798	12	US-11-131-479-99	Sequence 99, Appl
18	454	53.8	7798	12	US-11-131-479-100	Sequence 100, Appl
19	454	53.8	8442	12	US-11-131-479-106	Sequence 106, Appl
20	454	53.8	8442	12	US-11-131-479-107	Sequence 107, Appl

21	454	53.8	8450	12	US-11-131-479-104	Sequence 104, App
22	454	53.8	8450	12	US-11-131-479-105	Sequence 105, App
23	447.6	53.0	1027	12	US-11-155-478A-130	Sequence 130, App
24	401.8	47.6	629	9	US-11-137-807-18	Sequence 18, Appl
25	72.8	8.6	2430	7	US-10-649-457-3	Sequence 3, Appl
26	71	8.4	2295	7	US-10-649-457-1	Sequence 1, Appl
27	70.8	8.4	1521	12	US-11-129-442-22	Sequence 22, Appl
28	70.4	8.3	1683	12	US-11-131-479-37	Sequence 37, Appl
29	68.4	8.1	1566	12	US-11-131-479-33	Sequence 33, Appl
30	68.4	8.1	1566	12	US-11-131-479-35	Sequence 35, Appl
31	67.4	8.0	5278	12	US-11-124-602-2	Sequence 2, Appl
32	67.4	8.0	5304	12	US-11-124-602-1	Sequence 1, Appl
33	66.4	7.9	3624	7	US-10-755-092-6	Sequence 6, Appl
34	65.2	7.7	1494	8	US-10-763-712A-173	Sequence 173, App
35	64.8	7.7	1092	12	US-11-014-842A-40	Sequence 40, Appl
36	63.4	7.5	1497	12	US-11-131-479-24	Sequence 24, Appl
37	62.8	7.4	1218	9	US-11-096-568A-12913	Sequence 12913, A
38	62	7.3	1913	9	US-11-096-568A-23950	Sequence 23950, A
39	61.6	7.3	1815	9	US-11-096-568A-22463	Sequence 22463, A
40	61	7.2	1909	9	US-11-096-568A-24544	Sequence 24544, A
41	61	7.2	3468	7	US-10-755-092-2	Sequence 2, Appl
42	61	7.2	3468	7	US-10-755-092-4	Sequence 4, Appl
43	60.6	7.2	678	9	US-11-187-622-11	Sequence 11, Appl
44	60.2	7.1	2250	12	US-11-052-554A-532	Sequence 532, App
45	59.8	7.1	1325	9	US-11-096-568A-1077	Sequence 1077, Ap

ALIGNMENTS

RESULT 1
US-11-131-479-27
; Sequence 27, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein
US-11-131-479-27

Query Match	86.6%	Score 730.6;	DB 12;	Length 756;
Best Local Similarity	98.1%;	Pred. No. 6.1e-146;		
Matches 739;	Conservative 0;	Mismatches 14;	Indels 0;	Gaps 0;
Qy	83	AGCTCTGTCACCGAGGTGGAGACCTAGCTGCTGAGCATCATCCCGCGGCCCTCGAAG	142	
Db	4	AGCTCTGTCACCGAGGTGGAGACCTAGCTGCTGAGCATCATCCCGCGGCCCTCGAAG	63	
Qy	143	GCCGAGATGCCCGAGGTGGAGACCTGTTCCCGCGCAAGAACACCGACCTGGAGTG	202	
Db	64	GCCGAGATGCCCGAGGTGGAGACCTGTTCCCGCGCAAGAACACCGACCTGGAGTG	123	
Qy	203	CTGATGAGTGGCTGAAGACCGACCCCATCTGAGCCCCCTGACCAAGGGCATCTGGGC	262	
Db	124	CTGATGAGTGGCTGAAGACCGACCCCATCTGAGCCCCCTGACCAAGGGCATCTGGGC	183	

263 TTGCTGTTACCTTGAACGGTCCAGCGAGCGCGGCTGCGAGCGCCGCGCTTCTGTCAG 322
184 TTGCTGTTACCTTGAACGGTCCAGCGAGCGCGGCTTCTGTCAG 243
323 AACGCCCTGACCGCAACGGCGCCCAACAACTGACAGAGCGCGTGAAGCTGTACAGG 382
244 AACGCCCTGACCGCAACGGCGCCCAACAACTGACAGAGCGCGTGAAGCTGTACAGG 303
383 AAGCTGAAGAGGAGATCACCTTCCAGCGCGCCCAAGGAGATCACCTTGAAGCTGTACAGGCGCC 442
304 AAGCTGAAGAGGAGATCACCTTCCAGCGCGCCCAAGGAGATCACCTTGAAGCTGTACAGGCGCC 363
443 GGGCCCTTGGCCAGCTGATGGGCTGATCTTCAACAGGATGGCGCGCTGACCAACCGAG 502
364 GGGCCCTTGGCCAGCTGATGGGCTGATCTTCAACAGGATGGCGCGCTGACCAACCGAG 423
503 GTGGCCCTTGGCCAGCTGATGGGCTGATCTTCAACAGGATGGCGCGCTGACCAACCGAGC 562
424 GTGGCCCTTGGCCAGCTGATGGGCTGATCTTCAACAGGATGGCGCGCTGACCAACCGAGC 483
563 CACAGGAGATGGTGAACCAACCAACCCCTGATCAGGCAACGAGAACAGGATGGTGTG 622
484 CACAGGAGATGGTGAACCAACCAACCCCTGATCAGGCAACGAGAACAGGATGGTGTG 543
623 GCCAGCAACCGCCCAAGGCGCATGGAGCAGATGGCGCGGCGAGCAGCGAGCGCCGAG 682
544 GCCAGCAACCGCCCAAGGCGCATGGAGCAGATGGCGCGGCGAGCAGCGAGCGCCGAG 603
683 GCCATGAGTGGCGGCGAGCGCGCGAGCGAGTGGTGCAGGCGCATGGAGCGCGCGAGC 742
604 GCCATGAGTGGCGGCGAGCGCGCGAGCGAGTGGTGCAGGCGCATGGAGCGCGCGAGC 663
743 CACCCAGCAGCAGCGCGCGCTGAAGAACCACTTCTGAGAGAACCTTGCAGGCGCTTACAG 802
664 CACCCAGCAGCAGCGCGCGCTGAAGAACCACTTCTGAGAGAACCTTGCAGGCGCTTACAG 723
803 AAGCGCATGGCGGTGCGAGATGCGCGCTTCAAG 835
724 AAGAGGATGGCGGTGCGAGATGCGAGGTTCAAG 756

RESULT 2

US-11-479-69
; Sequence 69, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; PRIOR FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 69
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Open Reading Frame for M1 Gene from VR4760
US-11-479-69

Query Match 81.4%; Score 686.8; DB 12; Length 759;
Best Local Similarity 94.4%; Pred. No. 1.1e-136;
Matches 712; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY 85 CCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCGAGCGGCCCTTGAAGGC 144

Db 6 CTGCTGACAGAGTGGAAACATACGTGCTGAGCATCTGTCAGCGCGCCCTTGAAGGC 65
QY 145 CGAGATCGCCAGAGCTGGAGGACGTGTTTCGCGCGCAAGAACACCGACCTGGAGGTGCT 204
Db 66 CGAGATCGCCAGAGCTGGAGGACGTGTTTCGCGCGCAAGAACACCGACCTGGAGGCTT 125
QY 205 GATGGAGTGGCTGAAGACCAAGGCCCATCTCTGAGCCCTTGAACCAAGGGCATCTTGGGCTT 264
Db 126 GATGGAGTGGCTGAAGACCAAGGCCCATCTCTGAGCCCTTGAACCAAGGGCATCTTGGGCTT 185
QY 265 CGTGTTCACCTTCACTGCTGCGCGAGCGCGCTTGCAGCGCGCGCTTCTGTCAGAA 324
Db 186 CGTGTTCACCTTCACTGCTGCGCGAGCGCGCTTGCAGAGAGGCTTGCAGAGAAAGATTCGTGCGAA 245
QY 325 CGCCCTTGAACCGCAACCGCGACCCCAACAACTGACAAAGCGCGCTGAAGCTGTACAGAA 384
Db 246 CGCCCTTGAACCGCAACCGCGACCCCAACAACTGACAAAGCGCGCTGAAGCTGTACAGAA 305
QY 385 GCTGAAGAGGAGATCACTTTCACCGCGCAAGGAGATCAGCTGTAGCTTACAGCGCGG 444
Db 306 GCTGAAGAGAGAGATCACCTTTCACCGCGCAAGGAGATCAGCTGTAGCTTACAGCGCGG 365
QY 445 CGCCCTTGGCGAGCTGATGGGCTGATCTTCAACAGAAATGGCGCGCTGACCAACCGAGGT 504
Db 366 CGCCCTTGGCGAGCTGATGGGCTGATCTTCAACAGAAATGGCGCGCTGACCAACCGAGGT 425
QY 505 GGCCTTGGCGCTGCTGTCGCCACCTGCGAGCAGATCGCCGAGCAGCAGCAGCGCAGCCA 564
Db 426 GGCCTTGGCGCTGCTGTCGCCACCTGCGAGCAGATCGCCGAGCAGCAGCAGCGCAGCCA 485
QY 565 CAGGCGAGATGGTGACCAACCAACCCCTTGAAGGACGAGAACAGGATGGTGTGTCG 624
Db 486 CAGACAGATGGTGGCGCACCAACCAACCCCTTGAATCAGACAGAGAACAGGATGGTGTGTCG 545
QY 625 CAGCACCACCGCAAGGCCATGGAGCAGATGGCGCGCAGCAGCAGCGCGCGCGAGGC 684
Db 546 CAGCACCACCGCAAGGCCATGGAGCAGATGGCGCGCAGCAGCAGCGCGCGCGAGGC 605
QY 685 CATGGAGTGGCGCGCAGCGCAGGAGATGGTGCAGGCGCATGAGGACCATCGGACCCA 744
Db 606 CATGGAGTGGCGCGCAGCGCAGGAGATGGTGCAGGCGCATGAGGACCATCGGACCCA 665
QY 745 CCCAGCAGCAGCGCGCGCTGAAGAACGACCTGCTGAGAGAACCTGAGCGGCTTACCGAA 804
Db 666 CCCAGCAGCAGCGCGCGCTGAAGAACGACCTGCTGAGAGAACCTGAGCGGCTTACCGAA 725
QY 805 GCGCATGGCGGTGCGAGATGCGCGCTTCAAGTGA 838
Db 726 GAGAATGGCGGTGCGAGATGCGAGATTTCAAGTGA 759

RESULT 3

US-11-131-479-59
; Sequence 59, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; PRIOR FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 59
; LENGTH: 1050

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; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Open Reading Frame for the M2M1 Fusion from VR4755
US-11-131-479-59

Query Match      81.4%; Score 686.8; DB 12; Length 1050;
Best Local Similarity 94.4%; Pred. No. 1.1e-136;
Matches 712; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 85 CCTGCTGACCGAGGTGGAGACCTAGCTGTGAGCATCATCCAGCGGCCCTCTGAAGGC 144
Db 297 CTTGCTGACAGAGTGGAAACATACGTGTGAGCATGTGCTCCAGCGGCCCTCTGAAGGC 356
Qy 145 CGAGATCCCCAGAGGCTGGAGGAGCTGTTCGCGGCAAGAACACCGACCTGGAGGCTCT 204
Db 357 CGAGATCCCCAGAGCTGGAGGAGCTGTTCGCGGCAAGAACACCGACCTGGAGGCTCT 416
Qy 205 GATGAGTGGCTGAAGACCAAGCCCATCTGAGCCCTCTGACCAAGGGCATCTCTGGGCTT 264
Db 417 GATGAGTGGCTGAAGACCAAGCCCATCTGAGCCCTCTGACCAAGGGCATCTCTGGGCTT 476
Qy 265 CTTGTTACCTGACCTGCTGCGAGCGGCTGTGAGCGGCTGTGAGCGGCTGTCTGTCGAGAA 324
Db 477 CTTGTTACCTGACCTGCTGCGAGCGGCTGTGAGCGGCTGTGAGCGGCTGTCTGTCGAGAA 536
Qy 325 CGCCTGAACGGCAACGGCGACCCCAACAATGGACAAGCCGCTGAAGCTGTACAGGAA 384
Db 537 CGCCTGAACGGCAACGGCGACCCCAACAATGGACAAGCCGCTGAAGCTGTACAGGAA 596
Qy 385 GCTGAAGAGGAGATCACCTTTCCAGCGGCCCAAGGAGATCAGCTGTGAGCTACAGCGCGG 444
Db 597 GCTGAAGAGAGATCACCTTTCCAGCGGCCCAAGGAGATCAGCTGTGAGCTACAGCGCGG 656
Qy 445 CGCCTGCGCAGCTGATGCGGCTGTATCTAACAAGATGGGCGCTGTGACACCGAGGT 504
Db 657 CGCCTGCGCAGCTGATGCGGCTGTATCTAACAAGATGGGCGCTGTGACACCGAGGT 716
Qy 505 GGCCTTCGGCTGTGTGGCCACCTGCGAGCAGATCCCGACAGCCAGCCAGCCAGCCA 564
Db 717 GGCCTTCGGCTGTGTGGCCACCTGCGAGCAGATCCCGACAGCCAGCCAGCCAGCCA 776
Qy 565 CAGGAGATGTGTGACCAACCAACCCCTGATCAGGCAACAGGAAACAGATGTGTCTGGC 624
Db 777 CAGGAGATGTGTGACCAACCAACCCCTGATCAGGCAACAGGAAACAGATGTGTCTGGC 836
Qy 625 CAGCAACCGCAAGGCTCATGGAGCAGATGGCGGCAAGCAGAGCGCGCGGAGGC 684
Db 837 CAGCAACCGCAAGGCTCATGGAGCAGATGGCGGCAAGCAGAGCGCGCGGAGGC 896
Qy 685 CATGGAGTGGCCAGCCAGGCGCAGAGATGGTGCAGGCCATGAGGACCATCGGCACCCA 744
Db 897 CATGGAGTGGCCAGCCAGGCGCAGACAGATGGTGCAGGCCATGAGGACCATCGGCACCCA 956
Qy 745 CCCAGCAGCAGCGCGGCTTGAAGAACAGCCTGTGGAGAACCTGACAGGCTTACCAGAA 804
Db 957 CCCAGCAGCAGCGCGGCTTGAAGAACAGCCTGTGGAGAACCTGACAGGCTTACCAGAA 1016
Qy 805 GCGCATGGCGGTGCAGATGACGCGCTTCAAGTGA 838
Db 1017 GAGAAATGGCGGTGCAGATGACAGATTCAAGTGA 1050
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RESULT 4

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US-11-131-479-61
; Sequence 61, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vialta, Adrian
; APPLICANT: Wlocha, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
```

```
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 982
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Codon Optimized Segment 7 from VR4763
US-11-131-479-61
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Query Match      78.8%; Score 665.2; DB 12; Length 982;
Best Local Similarity 92.3%; Pred. No. 4.2e-132;
Matches 700; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 83 AGCCTGCTGACCGAGGTGGAGACCTAGCTGTGAGCATCATCCAGCGGCCCTCTGAAG 142
Db 4 AGCCTGCTGACCGAGGTGGAAACGTATGTCTCTATCGTGCAGCGGCCCTCTGAAG 63
Qy 143 GCCGAGATCGCCCAAGAGCTGGAGGAGCTGTTCGCCGCAAGAACACCGACCTGGAGGTG 202
Db 64 GCCGAGATCGCCCAAGAGCTGGAGGAGCTGTTCGCCGCAAGAACACCGACCTGGAGGCC 123
Qy 203 CTGATGAGTGGCTGAAGACAGGCCCATCTGTAGAGCCCTCTGACCAAGGGCATCTGTGGC 262
Db 124 CTGATGAGTGGCTGAAGACAGGCCCATCTGTAGAGCCCTCTGACCAAGGGCATCTGTGGC 183
Qy 263 TTGCTGTTCACTGACCGTGCAGCGGCGGCTGTGAGCGCGGCTGTGTCGAG 322
Db 184 TTGCTGTTCACTGACCGTGCAGCGGCGGCTGTGAGCGGCGGCTGTGTCGAG 243
Qy 323 AACCCCTGAACGGCAACGGCGACCCCAACAATGACAGAGGCGCTGAGCTGTACAGG 382
Db 244 AACCCCTGAACGGCAACGGCGACCCCAACAATGACAGAGGCGCTGAGCTGTACAGA 303
Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGGCCCAAGAGATCAGCTGTGATCAGCGCC 442
Db 304 AAGCTGAAGAGAGATCACCTTCCAGCGGCCCAAGAGATCAGCTGTGATCAGCGCC 363
Qy 443 GCGCCCTTGGCAGCTGCTGAGGCTGTATCTAACAAGATGGCGGCGGCTGACCAAGC 502
Db 364 GCGCCCTTGGCAGCTGCTGAGGCTGTATCTAACAAGATGGCGGCGGCTGACCAAGC 423
Qy 503 GTGSCCTTTCGGCTGTGTGCGCACCTGCGAGCAGATCGCCGACAGCAGCAGCCAGC 562
Db 424 GTGSCCTTTCGGCTGTGTGCGCACCTGCGAGCAGATCGCCGACAGCAGCAGCAGC 483
Qy 563 CACAGGAGATGTGTGACCAACCAACCCCTGTATCAGGCAACAGAAACAGATGTGTG 622
Db 484 CACAGAGATGTGTGCGCCACCAACCAACCCCTGTATCAGACACAGAGAACAGATGTGTG 543
Qy 623 GCCAGCACCAACCGCAAGGCCATGGAGCAGATGGCGGCGGAGCAGCAGCGCGCCGAG 682
Db 544 GCCAGCACCAACCGCAAGGCCATGGAGCAGATGGCGGCGGAGCAGCAGCGCGCCGAG 603
Qy 683 GCCATGGAGTGGCCAGCCAGGCGCAGATGGTGCAGGCCATGAGGCCATGAGGCCATCGG 742
Db 604 GCCATGGAGTGGCCAGCCAGGCGCAGACAGATGGTGCAGGCCATGAGGCCATCGG 663
Qy 743 CACCCAGCAGCAGCGCGGCTTGAAGAACAGCCTGTGTGAGAACCTGTGAGGCGCTTAC 802
Db 664 CACCCAGCAGCAGCGCGGCTTGAAGAACAGCCTTCTTGAAGAAATTTTGCAGACCTAT 723
Qy 803 AAGCGCATGGCGGTGCAGATGACGCGCTTCAAGTGAAC 840
Db 724 AACCGAATGGCGGTGCAGATGACACGATTCGAAGTGACC 761
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RESULT 5
US-11-131-479-79
; Sequence 79, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 79
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Optimized M1 Coding Region
US-11-131-479-79

Query Match      78.8%; Score 664.8; DB 12; Length 759;
Best Local Similarity 92.5%; Pred. No. 5.2e-132;
Matches 699; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCGAGCGGCCCTCTGAAG 142
Db 4 AGCCTGCTGACCGAGGTGGAGACCTATGTTCTCTATCTGTCGCCAGCGGCCCTCTGAAG 63

Qy 143 GCCGAGATCGCCGAGAGCTGGAGAGCGTGTTCGCCGCAAGAACACCGACCTGGAGGTG 202
Db 64 GCCGAGATCGCCGAGAGCTGGAGAGCGTGTTCGCCGCAAGAACACCGACCTGGAGGTG 123

Qy 203 CTGATGAGTGGCTGAGACAGCGCCCATCTCTGAGCGCCCTGACCAAGGGCATCTCTGGGC 262
Db 124 CTGATGAGTGGCTGAGACAGCGCCCATCTCTGAGCGCCCTGACCAAGGGCATCTCTGGGC 183

Qy 263 TTGCTGTTACCTTACCTGACCGTCCAGAGCGCGCCCTGACAGCGCGCGCTTCGTGCAG 322
Db 184 TTGCTGTTACCTTACCTGACCGTCCAGAGCGCGCCCTGACAGCGCGCGCTTCGTGCAG 243

Qy 323 AACGCCCTGAACGGGCAAGCGGACCCCAACATGAGCAAGGCGCGTGAAGCTGTACAGG 382
Db 244 AACGCCCTGAACGGGCAAGCGGACCCCAACATGAGCAAGGCGCGTGAAGCTGTACAGG 303

Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGCGCCCAAGAGATCAAGCTGAGCTACAGGCC 442
Db 304 AAGCTGAAGAGGAGATCACCTTCCAGCGCGCCCAAGAGATCAAGCTGAGCTACAGGCC 243

Qy 443 GCGCCCTTGGCGAGTGCATGGGCTGATCTACCAAGGATGGCGCGCTGACCAAGGCCAG 502
Db 364 GCGCCCTTGGCGAGTGCATGGGCTGATCTACCAAGGATGGCGCGCTGACCAAGGCCAG 423

Qy 503 GTGGCTTGGCGCTGGTGTGGCCACCTTGCAGCGAGATCGCGGACAGCGACCGACCGAGC 562
Db 424 GTGGCTTGGCGCTGGTGTGGCCACCTTGCAGCGAGATCGCGGACAGCGACCGACCGAGC 483

Qy 563 CACAGGAGATGGTGACCAACCAACCCCTGTATCAGGACAGGAAACAGGATGGTGTG 622
Db 484 CACAGGAGATGGTGACCAACCAACCCCTGTATCAGGACAGGAAACAGGATGGTGTG 543

Qy 623 GCCAGCACCAACCGCAAGGCCATGGAGCAGATGGCGCGGACAGCGAGCGCGCGCGAG 682
Db 544 GCCAGCACCAACCGCAAGGCCATGGAGCAGATGGCGCGGACAGCGAGCGCGCGCGAG 603

Qy 583 GCCATGGAGGTGGCCAGCGGACGAGGAGTGGTGTGAGGCCATGAGGACCATCGGCACC 742
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Db 604 GCCATGAGATGCCAGCGCCAGCCACAGCATGCTGAGGCGCATGAGAGCCATCGGCACC 663
Qy 743 CACCCAGCAGCAGCGCGCCCTTGAAGAACAGCACTCTCTGGAGAACCTTGCAGGCTTACCAG 802
Db 664 CACCCAGCAGCAGCGCGCCCTTGAAGATGATCTTCTTGAATAATTGCAGACCTATCAG 723

Qy 803 AACGGCATGGCGTGCAGATGCAGCGCTTCAAGTGA 838
Db 724 AAACGAATGGGGTGCAGATGCAACGATTCAAGTGA 759

RESULT 6
US-11-131-479-28
; Sequence 28, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 28
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein
US-11-131-479-28

Query Match      70.5%; Score 594.6; DB 12; Length 756;
Best Local Similarity 86.9%; Pred. No. 3.8e-117;
Matches 654; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

Qy 83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCGAGCGGCCCTCTGAAG 142
Db 4 AGCTGCTGACAGAGGTGGAGACGTACGTGCTGTCCATCATTCCTCAGGCCCTCTGAAG 63

Qy 143 GCCGAGATCGCCGAGAGCTGGAGAGCGTGTTCGCCGCAAGAACACCGACCTGGAGGTG 202
Db 64 GCCGAGATCGCCGAGAGCTGGAGAGCGTGTTCGCCGCAAGAACACCGACCTGGAGGTG 123

Qy 203 CTGATGAGTGGCTGAAGACAGCGCCCATCTCTGAGCGCCCTGACCAAGGGCATCTCTGGGC 262
Db 124 CTGATGAGTGGCTGAAGACAGCGCCCATCTCTGAGCGCCCTGACCAAGGGCATCTCTGGGC 183

Qy 263 TTGCTGTTACCTTACCTGACCGTCCAGAGCGCGCCCTGACAGCGCGCGCTTCGTGCAG 322
Db 184 TTGCTGTTACCTTACCTGACCGTCCAGAGAGGCGCTTCGAGCGGAGGAGGTTCGTTCAG 243

Qy 323 AACGCCCTGAACGGGCAAGCGGACCCCAACATGAGCAAGGCGCGTGAAGCTGTACAGG 382
Db 244 AACGCCCTGAACGGGCAAGCGGATCCCAACATGAGTAAGGCGGTGAAGCTGTATAGA 303

Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGCGCCCAAGAGATCAAGCTGAGCTACAGGCC 442
Db 304 AAGCTGAAGAGGAGATCACATTTATGCGCCCAAGAGATATCGCTGAGCTACAGTGCC 363

Qy 443 GCGCCCTTGGCGAGTGCATGGGCTGATCTACCAAGGATGGCGCGCTGACCAAGGCCAG 502
Db 364 GCGCCCTTGGCGCTTTCATGGGCTGATATACCAAGAAATGGGCGCGCTTACTACAGAG 423

Qy 503 GTGGCTTGGCGCTGGTGTGGCCACCTGCGAGCAGATCGCGGACAGCGACCGACCGAGC 562
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Db 424 GTAGCTTTGGCTGGTCTGGCCACTTGGCAGCAGATCGCCGACTCTCAGCATAGATCT 483
Qy 563 CACAGCAGATGGTGACCAACCAACCCCTGTATGATGAGCAGGAGATGGTGTG 622
Db 484 CACAGCAGATGGTGACGACTTACAAACCCCTGTATGAGCAGGAGATGGTGTG 543
Qy 623 GCCAGCACCGCCCAAGGCCATGGAGCAGATGGCCGCGCAGCAGCAGCCGCGAG 682
Db 544 GCCTCTACTACCGCCCAAGGCCATGGAGCAGATGGCCGCGCAGCAGTGTAGCAGCCGCGAG 603
Qy 683 GCCATGGAGTGGCCAGCAGCCAGCAGCAGATGGTGAGGCGCATGAGAACCATGGCACC 742
Db 604 GCCATGGAGTGGCCAGCAGCCAGCAGATGGTGAGGCGCATGCGAACCATGGCAGT 663
Qy 743 CACCCACAGCAGCAGCCGCGCTGAAGAACGACCTGTCTGGAGAACCTTCAAG 835
Db 664 CACCCCTCAGCTCTGCGCGCTGAAGAACGACCTGTCTGGAGAACCTTCAAG 723
Qy 803 AAGCGCATGGCGTGCAGATGCGCGCTTCAAG 835
Db 724 AAGAGATGGCGTACAGATGACAGAGTTCAAG 756

RESULT 7

US-11-131-479-26
; Sequence 26, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 26
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein
US-11-131-479-26

Query Match 57.8%; Score 488; DB 12; Length 756;
Best Local Similarity 78.1%; Pred. No. 1.4e-94;
Matches 587; Conservative 0; Mismatches 165; Indels 0; Gaps 0;
Qy 83 AGCTGTCTGACCGAGGTGGAGACCTTACGTCTGAGCATCATCCCGAGCGGCCCTGAAG 142
Db 4 AGCTGTCTAAAGAGTGGAAACCTATGTCTCTAGTATCATCTTCTAGCGGCCCTTAAA 63
Qy 143 GCCAGATGCCCCAGAGCTGGAGAGCGTGTTCGCCGCGCAAGAACACCGACCTGGAGTG 202
Db 64 GCCGAAATCGCTCAGCGGCTCGAGGATGTTTTTGGCGGCAAGAACACCGACCTGGAGTA 123
Qy 203 CTGATGGAGTGGCTGMAAGACAGCCCATCTGTAGCCCTCTGACCAAGGGATCCTGGC 262
Db 124 TTGATGGAGTGGCTGMAAGACAGCCCATCTGTAGCCCTCTGACCAAGGGATCCTGGC 183
Qy 263 TTCGTGTTTACCTTACCGTCCAGCGAGCGGCGCTTGCAGCGCGCGCTTGTGCGAG 322
Db 184 TTCGTGTTTACCTTACCGTCCAGCGAGCGGCGCTTGCAGCGCGCGCTTGTGCGAG 243
Qy 323 AACGCCCTGAAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCA 382
Db 244 AACGCCCTTAAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCA 303

Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGGGGCCAAGAGATCAGCTGAGCTACAGCGCC 442
Db 304 AAATTAAGCGGAGATAA CTTTCCATGGAGGCAAGGAGATCTCCCTGTCTTACTTGA 363
Qy 443 GGCGCCCTGGCAGCTGCATGGGCTGATCTTAACAAAGATGGGCGCGCTGACCAACCGAG 502
Db 364 GGTGCTCTCGCGTGTATGGGACTTATCTTACAAACCGAATGGGCGCGCTGACCAACGAA 423
Qy 503 GTGGCCTTCCGCGTGTGGCCACCTGGCAGCAGATCGCCGACAGCAGCAGCAGCGCAGC 562
Db 424 GTGGCTTTGGGCTGGTGGCGCAACTTGGGAA CAGATTGCTGACAGT CAGACCGGTCC 483
Qy 563 CACAGCAGATGGTGACCAACCAACCCCTGTATGAGGCAACGAGAACAGATGGTGTG 622
Db 484 CACCGTCAATGGT CACCAACCAATCCGCTGATTAGACATGAANAATCGCATGGTTCTA 543
Qy 623 GCCAGCACCGCCCAAGGCCATGGAGCAGATGGCCGCGCAGCAGCAGCGGCCCGAG 682
Db 544 GCATCAACTACAGCCAAAGCAATGGAA CAAATGGCCGGAAGCTCCGAGCAGGCTGCCGAG 603
Qy 683 GCCATGGAGTGGCCAGCGGCCAGCAGATGGTGAGGCGCATGAGGACCATCGGCACC 742
Db 604 GCGATGGAGTGGCGTCCCGAGCCAGACAGATGGTACAGGCTATGAGAACTATCGGTACG 663
Qy 743 CACCCACAGCAGCAGCGCGGCTTGAAGAACGACCTGTCTGGAGAACCTTGCAGGCGCTTACCAG 802
Db 664 CACCAAGTCTTTCAGCTGGGCTGAGAGATGATCTTCTTGGAACTCTGAGGCGCTTACCNA 723
Qy 803 AAGCGCATGGCGTGCAGATGCGCGCTTCA 834
Db 724 AAGCGGATGGCGTCCAGATGACAGATTTAA 755

RESULT 8

US-11-131-479-3
; Sequence 3, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 3
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Influenza A virus
US-11-131-479-3
Query Match 56.4%; Score 476.4; DB 12; Length 1027;
Best Local Similarity 76.8%; Pred. No. 4e-92;
Matches 582; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

Qy 83 AGCTGTCTGACCGAGGTGGAGACCTTACGTCTGAGCATCATCCCGAGCGGCCCTGAG 142
Db 29 AGTCTTCTAACCGAGGTGCAAGCTACTCTTCTATCTATCTCCGTCAGGCGCCCTCAA 88
Qy 143 GCCAGATGCCCGAGCGTGGAGAGCGTGTTCGCCGCGCAAGAACACCGACCTGGAGTG 202
Db 89 GCCAGATGCCCGAGCGTGGAGAGCGTGTTCGCCGCGCAAGAACACCGACCTGGAGTG 148
Qy 203 CTGATGGAGTGGCTGAAAGACAGGCCCATCTGTAGCCCTCTGACCAAGGGGATCCTGGC 262

Db 149 CTCATGAATGGCTAAAGACAGACCAGTCTCTGTCACTCTGACTAAGGGATTTTAGGA 208
Qy 263 TTCGTGTTTACCTTGACCGTGCCAGGAGCGCGCTGCGAGCCGCCCGCTTCGTGCAG 322
Db 209 TTTGTGTTTACCGTCTACCGTGCCAGTGAGCGAGGACTGCGAGCGTGTGTCAG 268
Qy 323 AACGCCCTGAACGGCAAGCGGAGCCCAACAACTATGACACAGGCGGTGAAGCTGTACAG 382
Db 269 AATGCCCTTATGGGAACGGGGATCCAAATAACTATGACAAAGCAGTTAAACTGTATAGG 328
Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGGCCCAAGGAGATCAACCTTGAGCTACAGGCC 442
Db 329 AAGCTCAAGAGGGAGATAACATTCATGGGGCCAAAGAAATCTCACTCAGTTATCTGCT 388
Qy 443 GGGCCCTTGGCCAGCTGCGATGGGCTGATCTTACACAGGATGGCGCGCTGACCAACCGAG 502
Db 389 GGTGCACTTGGCACTTGTATGGGCTCATATACAAAGGATGGGGCTGTGACCACTGAA 448
Qy 503 GTGGCCTTGGCCTGTGTGGCCACCTGCGAGCAGATCGCCGACAGCAGCAGCCGAGC 562
Db 449 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAAACAGATTGCTGACTCCCAAGCATCGTCT 508
Qy 563 CACAGGAGATGGTGACCAACCAACCCCTGTATCAGGACGAGAACAGGATGGTGTG 622
Db 509 CATAGGCAATGGTGACAAACCAATCCACTATTCAGATGAGAACAGATGGTTTAA 568
Qy 623 GCCAGCACCGCAAGGCCATGGAGCAGATGGCCGCGCAGCAGCAGCGCCGAG 682
Db 569 GCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGGATCGAGTGAAGCAGCAGAG 628
Qy 683 GCCATGAGGTGGCCAGCCAGCCAGGAGATGGTGAGGCCATGAGGACCATCGGCACC 742
Db 629 GCCATGAGGTGTGTAGTCAGGCTAGACAAATGGTGCAAGCGATGAGAACCATTTGGGACT 688
Qy 743 CACCCAGCAGCAGCGCGGCTGAAGAACCACTGCTGGAGAACCTGCGAGGCTTACCAG 802
Db 689 CATCTAGCTCCAGTGTGTGTTTGAATAATGATCTTTTGAATAATTGACGGCTATCAG 748
Qy 803 AAGCGCATGGCGTGCGAGATGCAGCGCTTCAAGTGAAC 840
Db 749 AACGAATGGGGTGCGAGATGCACACGGTTCAAGTGATC 786

RESULT 9

US-11-131-479-45
; Sequence 45, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 1305
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Influenza A Virus M1 Fused to Synthetic HBcAg
US-11-131-479-45

Query Match 56.0%; Score 473; DB 12; Length 1305;
Best Local Similarity 76.8%; Pred No. 2.1e-91;
Matches 578; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

Qy 83 AGCCTGTCACCGAGGTGGAGACTAGCTGCTGAGCATCATCCCGAGCGGCCCTGAAG 142
Db 4 AGTCTTTCTAACCGAGGTGGAACGTACGTACTCTATCATCTCCGTCAGCGCCCTCAAA 63
Qy 143 GCCAGATGCCCAGAGGCTGGAGGAGCTGTCGCCGGCAAGAACACACCGACCTGGAGGTG 202
Db 64 GCCAGATGCCACAGAGACTTGAAGATGCTTTGCGAGGGAAGAACACTGATCTTGAGTT 123
Qy 203 CTGATGAGTGGCTGAAGACACAGCCCATCTCTGAGCCCTCTGACCAAGGGAGATCCTGGCG 262
Db 124 CTCATGGAATGGCTAAAGACAAGACCAATCTCTGTACACTCTGACTAAGGGGATTTAGGA 183
Qy 263 TTGCTGTTTACCTGACCGTGGCCAGGAGCGCGGCTGCGAGCGGCCCTCTGTCGAG 322
Db 184 TTTGTGTTTACGCTTCCCGTGGCCAGTGAAGAGGACTGCGAGCGTGAACGCTTTGTCAA 243
Qy 323 AACGCCCTGAACGGCAACGGCGACCCCAACAACTATGGAACAGGCGGTGAAGCTGTACAGG 382
Db 244 AATGCCCTTAAATGGGAACGGGGATCCAAATAACTATGGAACAGGATTTAACTGTATAGG 303
Qy 383 AAGCTGAAGAGGAGATCACCTTTCAGGGCCCAAGAGAGATCAGCTTGAGCTACAGGCC 442
Db 304 AAGCTCAAGAGGAGATTAACATTTCCATGGGGCCAAAGAAATCTCACTCAGTTATCTGCT 363
Qy 443 GGGCCCTGCGCAGCTGCGATGGCGCTGATCTAACAGAGTGGCGCGCTGACCAACCGAG 502
Db 364 GGTGCACTTGGCAGTTGTATGGGCTCATATACAAAGGATGGGGCTGTGACCACTGAA 423
Qy 503 GTGGCTTTCGGCTGGTGTGCGCACCTGCGAGCAGATCGCCGACAGCCAGCAGCCGAGC 562
Db 424 GTGCAATTTGGCTGGTGTATGTGCAACTGTGAACAGATTTGCTGACTCCAGCATCGTCT 483
Qy 563 CACAGGAGATGGTGACCAACCAACCCCTCTGATCAGGCACGAGAACAGATGGTGTG 622
Db 484 CATAGGCAATGGTGACAAACCAATCCACTAATCAGACATGAGAACAGATGGTTTAA 543
Qy 623 GCACGACACCGCCAGGCGCATGAGCAGATGGCGGAGCAGCAGCGAGCGGCCGAG 682
Db 544 GCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGGATCGAGTGAAGCAGCAGAG 603
Qy 683 GCCATGAGGTGGCCAGCGCAGGCGAGCAGATGGTGAGGCCATGAGGACCATCGGCACC 742
Db 604 GCCATGAGGTGCTAGTCTAGGCTAGACAAATGGTGCAAGGATGAGAACCATTTGGGACT 663
Qy 743 CACCCAGCAGCAGCGCGCTTGAACACGACCTGCTGGAGAACCTTGGAGGCTTACCAG 802
Db 664 CATCTAGCTCCAGTGTGCTGTTGAAAATGATCTTCTTGAATAATTTCAGGCGCTATCAG 723
Qy 803 AAGCGCATGGCGTGCGAGATGCAGCGCTTCAAG 835
Db 724 AACGAATGGGGTGCGAGATGCAACGGTTCAAG 756

RESULT 10

US-11-155-478A-131
; Sequence 131, Application US/11155478A
; Publication No. US20060014140A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE Laval
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 174

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 987
; TYPE: DNA
; ORGANISM: human Influenza A virus
; FEATURE:
; LOCATION: (1)...(987)
; NAME/KEY: gene
; OTHER INFORMATION: human Influenza A virus
; OTHER INFORMATION: strain A/Charlottesville/31/95 (H1N1)
; OTHER INFORMATION: accession number AF398876
US-11-155-478A-131

Query Match 54.5%; Score 460.4; DB 12; Length 987;
Best Local Similarity 75.5%; Pred. No. 9.8e-89;
Matches 572; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

```
Qy 83 AGCTGTGACCGAGGTGGAGACCTAGTGTGTGAGCATCATCCCGAGCGGCCCTCGAAG 142
Db 4 AGTCTTCTAACCGAGGTGGAACGTACGTTCTCTATCGTCCGTCAGGCCCTCAA 63

Qy 143 GCCGAGATCGCCGAGAGCTGGAGAGCTGTTGCGCGGCAAGAACACCGACCTGGAGTG 202
Db 64 GCCGAGATCGCAGAGACTTGAAGATGTCTTGTCTGGAAGAAACACCGATCTTGAGGCT 123

Qy 203 CTGATGAGTGGCTGAAGACAGGCCCATCTGTAGCGCCCTGACCAAGGGCATCTGGGC 262
Db 124 CTCATGAGTGGCTTAAGACAAGACCGATCTCTACCTGTAGTAAGGGATTTAGGA 183

Qy 263 TTCGTGTTACCCCTGACCGTCCAGCGAGCGCGCTGACGCGCCCGCTTCGTGCGAG 322
Db 184 TTTGTGTTACCGTCCAGTCCCGTCCAGTGGAGGACTGACGCTAGAGCGCTTTGTCAA 243

Qy 323 AACGCCCTGAAGCGGAGATCACCTTCCAGCGGCCAAGGAGATCAGCTGAGCTACAGCGCC 442
Db 244 AATGCCCTTAATGGGAATGGGGATCCAAATAACATGGAACAGACAGTAAACTGTATAGA 303

Qy 383 AAGCTGAAGCGGAGATCACCTTCCAGCGGCCAAGGAGATCAGCTGAGCTACAGCGCC 442
Db 304 AAGCTTAAGCGGAGATTAATTCATGGGGCCAAAGAAATAGCACTAGTTATCTGCT 363

Qy 443 GCGCCCTTGGCGTGCATGGGCTGATCTTACACAGAGATGGCGCGCTGACACCGAG 502
Db 364 GGTGCACTTGCAGTTGATGGGCTCATATACACAGAGATGGGGCTGTGACCAACGAA 423

Qy 503 GTGGCTTGGCGCTGTGTCGCCCATCTGCAGCAGATTCGCCGACAGCAGCGCAGC 562
Db 424 TCAGCATTTGGCCTGATATGCGCAACCTGTGAACAGATTTGCTGACTCCCGACATAAGTCT 483

Qy 563 CACAGGAGATGGTGACCAACACCCCTGATCAGGCACGAGAACAGGATGGTGTG 622
Db 484 CATAGGCAATGGTAACAAACCAATCCATTAAGACATGAGAACAGAAATGGTCTG 543

Qy 623 GCCAGCACACCGCCAGGCGCATGGAGCAGATGGCGCGCAGCAGCGCGCCGAG 682
Db 544 GCCAGCACTACAGCTAAGCTATGGAGCAATGGCTGGATCGAGTGAACAGCAGCTGAG 603

Qy 683 GCCATGAGGTGGCGCAGCGCAGGATGGTGTGAGGCCATGAGGACCATCGGCACC 742
Db 604 GCCATGAGGTGGCTAGTCAGCGCAGGCAATGGTGCAGGCAATGAGAGCCATTGGGACT 663

Qy 743 CACCCAGCAGCGCGGCTGAAGAACCACTGCTGGAGAACCTGCGAGGCTTACCAG 802
Db 664 CATCTAGCTCTAGCAGCTGGTCTGAAATAATGATCTCTTGAATAATTTGCAGGCTATCAG 723

Qy 803 AAGCGCATGGCGTGCAGATGCAGCGCTTCAAGTGAAC 840
Db 724 AAACGATGGGGTGCAGATGCAACGATTTCAAGTGATC 761
```

RESULT 11

US-11-131-479-60

; Sequence 60, Application US/11131479

; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60
; LENGTH: 982
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Open Reading Frame for Fragment 7 from VR4756
US-11-131-479-60

Query Match 53.8%; Score 454; DB 12; Length 982;
Best Local Similarity 74.9%; Pred. No. 2.2e-87;
Matches 568; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

```
Qy 83 AGCTGTGACCGAGGTGGAGACCTAGTGTGTGAGCATCATCCCGAGCGGCCCTCGAAG 142
Db 4 AGCTTCTTAACCGAGGTGGAACGTATGTTCTCTATCGTTCATCAGGCCCTCAA 63

Qy 143 GCCGAGATCGCCGAGAGCTGGAGAGCTGTTGCGCGGCAAGAACACCGACCTGGAGTG 202
Db 64 GCCGAGATCGCAGAGACTTGAAGATGTCTTGTCTGGGAAAACACAGATCTTGAGGCT 123

Qy 203 CTGATGAGTGGCTGAAGACAGCGCCCATCTGTAGCGCCCTGACCAAGGGCATCTGGGC 262
Db 124 CTCATGGAATGGCTTAAGACAAGACCAATCTGTACCTCTGACTAAGGGATTTGGGG 183

Qy 263 TTCGTGTTACCTGACCGTGCAGCGCGGCTGACGCGCCCGCTTCGTGCGAG 322
Db 184 TTTGTGTTACCGTCCAGTCCCGTGCAGTGGAGGACTGCGAGCGTAGACGCTTTGTCAA 243

Qy 323 AACGCCCTGAACCGCAACCGGACCCCAACATGACAGCGCCGTGAAGCTGTACAGG 382
Db 244 AATGCCCTCAATGGGAATGGGGATCCAAATAACATGGAACAGAGATTAACATATAGA 303

Qy 383 AAGCTGAAGCGGAGATCACCTTCCAGCGGCCAAGGAGATCAGCTGAGCTACAGCGCC 442
Db 304 AACTTAAGAGGGAGATTAATTCATGGGGCCAAAGAAATAGCACTAGTTATCTGCT 363

Qy 443 GCGCCCTGCGCAGCTGCATGGGCTGATCTTAAACAGGATGGCGCGCTGACACCGAG 502
Db 364 GGTGCACTTGCAGTTGCATGGGCTCATATACAAAGAAATGGGGCTGTAAACCACTGA 423

Qy 503 GTGGCTTGGCGCTGTGTCGCCCATCTGCAGCAGATTCGCCGACAGCAGCGCAGC 562
Db 424 GTGGCTTGGCGCTGTGTCGCAACATGTGAACAGATTTGCTGACTCCCGACAGGTCT 483

Qy 563 CACAGGAGATGGTGACCAACACCCCTGATCAGGCACGAGAACAGGATGGTGTG 622
Db 484 CATAGGCAATGGTGGCAACCAACATTCATTAAGGGCATGAGAACAGAAATGGTGTG 543

Qy 623 GCCAGCACACCGCCAGGCGCATGGAGCAGATGGCGCGCAGCAGCGCGCCGAG 682
Db 544 GCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGGATCGAGTGAACAGCAGCTGAG 603

Qy 683 GCCATGAGGTGGCGCAGCGCAGGATGGTGTGAGGCCATGAGGACCATCGGCACC 742
Db 604 GCCATGGAATTTGCTAGTCAGCGCAGGCAATGGTGCAGGCAATGAGAGCCATTGGGACT 663

Qy 743 CACCCAGCAGCAGCGCGCTTGAAGAACCACTGCTGGAGAACCTGCGAGGCTTACCAG 802
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Db 664 CATCTAGCTCCAGTGTGGTCTAAAGATGATCTTCTTGAAATTTGCAGACCTATCAG 723
Qy 803 AAGCGCATGGCGTCGACAGATGCGAGCGCTTCAAGTGAAC 840
Db 724 AAACGAATGGGGTGCAGATGCAACGATTCAAGTGACC 761

RESULT 12
US-11-131-479-95
; Sequence 95, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95
; LENGTH: 4822
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4764, Ligation of VR4756 RV-Sali into VR10682 RV
US-11-131-479-95

Query Match 53.8%; Score 454; DB 12; Length 4822;
Best Local Similarity 74.9%; Pred. No. 2e-87;
Matches 568; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

Qy 83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCGAGCGGCCCTCGAAG 142
Db 817 AGCCTTCTAACCGAGGTGGAACGATGTTCTCTATCGTTCCATCAGCGCCCTCAA 876
Qy 143 GCCAGATCGCCAGAGCGTGGAGAGCGTGTTCGCGGCAAGAACACCGACCTGGAGTG 202
Db 877 GCCAAATCGCGCAGAGACTTGAAGATGTTCTTCTGCGGAAAAACAGATCTTGAAGCT 936
Qy 203 CTGATGAGTGGCTGAAGACCGAGCCCATCTGAGCCCTTGACCAAGGCGATCCTGGC 262
Db 937 CTCATGGAATGGCTAAAGACAAGACCAATCTGTACCTCTGACTAAGGGGATTTTGGG 996
Qy 263 TTGCTGTTACCTTCAGCGTCCCGAGGAGCGCGCCCTGACGCGCCCGCTTCGTGCAG 322
Db 997 TTTGTGTTACGCTCACCGTGCCAGTGAGCGAGACTGTCAGCTAGACGCTTTGTCAA 1056
Qy 323 AACGCCCTGAACGGCAACGGCGAACCCCAACAATGACAGAGGCGGTGAAGCTGTACAG 382
Db 1057 AATGCCCTCAATGGGAATGGGGATCCAAATAACATGACAGAGCAGTAAACTATATAGA 1116
Qy 383 AAGCTGAAGGGAGATCACCTTCCAGCGCCCAAGGAGATGGCGCGCTGACCATCAGCGCC 442
Db 1117 AAATTAAGAGGGAGATTACATTCATGGGGCCAAAGAAATAGCACTCAGTTATTCTGCT 1176
Qy 443 GCGCCCTTGGCGACGTGCATGGGCTGATCTACACAGAGATGGCGCGCTGACCAACCGAG 502
Db 1177 GGTGCACTTGCAGTTGCATGGGCTCATATACACAGAAATGGGGGCTGTAAACCACTGAA 1236
Qy 503 GTGCGCTTGGCGCTTGGTGTGCGCCACTGCGAGCAGATGCGCGACAGCGCAGCACCGAGC 562
Db 1237 GTGCGCTTTGGCGCTTGGTGTGCAACATGTGAACAGATTGCTGACTCCCAAGCAGGTCT 1296
Qy 563 CACAGGAGATGGTGAACCAACCAACCCCTGATCAGGCACAGAAAGAGATGGTGTG 622
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Db 1297 CATAGCAATGGTGCACAAACCAATCCATTAAAGCATGAGAACAAGATGTTTGT 1356
Qy 623 GCAGACCAACCGCCCAAGGCCATGAGAGATGGCCGGCAGAGCCAGCAGCAGCGCCGAG 682
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Qy 683 GCCATGGAGTGGCCAGCAGCAGCGCAGATGGTGCAGCCATGAGGCCATTCGGCACC 742
Db 1417 GCCATGGAATTTGCTAGTCAGGCCAGGCAATGGTGCAGCAATGAGCCATTGGGACT 1476
Qy 743 CACCCAGCAGCAGCGCCCGCTTGAAGAACGACCTGCTGGAGAACCTGCGAGGCTACACAG 802
Db 1477 CATCTAGCTCCAGTGTGCTTAAAGATGATCTTCTTGAAATTTGCAGACCTATCAG 1536
Qy 803 AAGCGCATGGCGTGCAGATGCGAGCGCTTCAAGTGAAC 840
Db 1537 AAACGAATGGGGTGCAGATGCAACGATTCAAGTGACC 1574

RESULT 13
US-11-131-479-101
; Sequence 101, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 101
; LENGTH: 5161
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4770, M2 Insert Replacing WNV Insert in VR6430
US-11-131-479-101

Query Match 53.8%; Score 454; DB 12; Length 5161;
Best Local Similarity 74.9%; Pred. No. 2e-87;
Matches 568; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

Qy 83 AGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCGAGCGGCCCTCGAAG 142
Db 1150 AGCCTTCTAACCGAGGTGGAACGATGTTCTCTATCGTTCCATCAGCGCCCTCAA 1209
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Db 1210 GCCAAATCGCGCAGAGACTTGAAGATGTTCTTCTGCGGAAAAACAGATCTTGAAGCT 1269
Qy 203 CTGATGAGTGGCTGAAGACCGAGCCCATCTGAGCCCTTGACCAAGGCGATCCTGGGC 262
Db 1270 CTCATGGAATGGCTAAAGACAAGACCAATCTGTACCTCTGACTAAGGGGATTTTGGG 1329
Qy 263 TTGCTGTTACCTTCAGCGTGGCGCGCGCTGAGCGCGCGCTGAGCGCGCCCTTCGTGCAG 322
Db 1330 TTTGTGTTACGCTCACCGTGCCAGTGAAGGAGACTGCGCGGTAGACGCTTTGTGCTCAA 1389
Qy 323 AACGCCCTGAACGGCAACGGCGAACCCCAACAATGACAGAGGCGGTGAAGCTGTACAGG 382
Db 1390 AATGCCCTCAATGGGAATGGGGATCCAAATAACATGACAGAGCAGTTAACTATATAGA 1449
Qy 383 AAGCTGAAGAGGAGATCACCTTCCAGCGCGCCCAAGGAGATCAGCCTGAGCTACAGCGCC 442
Db 1450 AAATTAAGAGGGAGATTACATTCATTCATGGGGCCAAAGAAATAGCACTCAGTTATTCTGCT 1509
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[illegible]

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Job time : 385.719 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2006, 23:02:13 ; Search time 190.994 Seconds
(without alignments)
8767.110 Million cell updates/sec

Title: US-10-729-830-5
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Gapop 10.0 , Gapext 1.0

Searched: 130357 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	764	81.1	4023	3	US-08-809-513A-8
2	761.8	80.9	6802	3	US-08-809-513A-6
3	695.8	73.9	1027	6	PCT-US95-12357A-3
4	647.4	68.7	1023	3	US-09-506-286B-1
5	647.4	68.7	1023	3	US-09-762-861B-1
6	647.4	68.7	1023	3	US-10-065-133A-1
7	647.4	68.7	1023	3	US-10-434-811A-1
8	644.6	68.4	1023	3	US-09-506-286B-4
9	644.6	68.4	1023	3	US-09-762-861B-4
10	644.6	68.4	1023	3	US-10-065-133A-4
11	644.6	68.4	1023	3	US-10-434-811A-4
12	637.2	67.6	756	3	US-09-506-286B-3
13	637.2	67.6	756	3	US-09-762-861B-3
14	637.2	67.6	756	3	US-10-065-133A-3
15	637.2	67.6	756	3	US-10-434-811A-3
16	634.4	67.3	756	3	US-09-506-286B-6
17	634.4	67.3	756	3	US-09-762-861B-6
18	634.4	67.3	756	3	US-10-065-133A-6
19	634.4	67.3	756	3	US-10-434-811A-6
20	632.6	67.2	816	3	US-09-311-784A-13
21	79	8.4	290	3	US-10-131-827-8418
22	77.6	8.2	1097	3	US-09-832-129-21
23	77.2	8.2	1069	3	US-09-372-422A-7
24	76.8	8.2	569	3	US-09-461-325-44

25	76.8	8.2	569	3	US-10-012-542-44	Sequence 44, Appl
26	76.8	8.2	569	3	US-10-115-123-44	Sequence 44, Appl
27	76.8	8.2	3080	3	US-09-099-041A-25	Sequence 25, Appl
28	76.8	8.2	3080	3	US-09-245-281-25	Sequence 25, Appl
29	76.8	8.2	3080	3	US-09-207-359B-25	Sequence 25, Appl
30	76.8	8.2	3080	3	US-09-340-620A-25	Sequence 25, Appl
31	76.8	8.2	3080	3	US-09-865-364-25	Sequence 25, Appl
32	76.8	8.2	3080	3	US-09-728-721-25	Sequence 25, Appl
33	76	8.1	1733	3	US-09-073-569-1	Sequence 1, Appl
34	75.8	8.0	990	3	US-09-800-729-79	Sequence 79, Appl
35	75.8	8.0	1934	3	US-08-776-844-1	Sequence 1, Appl
36	75.8	8.0	1934	3	US-09-909-325-1	Sequence 1, Appl
37	75.8	8.0	1934	3	US-09-909-326-1	Sequence 1, Appl
38	75.8	8.0	1985	3	US-09-907-794A-212	Sequence 212, App
39	75.8	8.0	1985	3	US-09-905-125A-212	Sequence 212, App
40	75.8	8.0	1985	3	US-09-902-775A-212	Sequence 212, App
41	75.8	8.0	1985	3	US-09-906-700-212	Sequence 212, App
42	75.8	8.0	1985	3	US-09-903-603A-212	Sequence 212, App
43	75.8	8.0	1985	3	US-09-904-920A-212	Sequence 212, App
44	75.8	8.0	1985	3	US-09-909-064-212	Sequence 212, App
45	75.8	8.0	1985	3	US-09-905-381A-212	Sequence 212, App

ALIGNMENTS

RESULT 1

US-08-809-513A-8
; Sequence 8, Application US/08809513A
; Patent No. 6524588
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
; TITLE OF INVENTION: Method
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising
; NUMBER OF SEQUENCE ADDRESSES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESS: NORRIS MCLAUGHLIN & MARCUS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Gateway Pentium II
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,513A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03663
; FILING DATE: 18-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94115505.3
; FILING DATE: 30-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Hobom 9832-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4023 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

Db 394 TTCTGCTGGTGCACCTTGCCAGTTGTATGGGCTCATATACACAGGATGGGGTGTGAC 453
QY 472 CACUGAAGUGCAUUGGCCUGGUAUGGCAACGUGGAAACAGAUUGCUGACUCCCGCA 531
Db 454 CACTGAGTGGCATTTGGCTGGTATGTGCAACCTGTGAACAGATTGTCTCTCCCGCA 513
QY 532 UCGGUCUCAAAGGCAAAUGGUGACAAACCAACCAACCAACCAACCAACCAACCAAC 591
Db 514 TCGGTCTCATAGGCAAAATGGTGACAAACCAACCAACCAACCAACCAACCAACCA 573
QY 592 GGUUUUAGCCAGCAUACAGCUAAGGCUUAGAGCAAAUGGCAAAUGGCUAGGAGCAAGC 651
Db 574 GGTTTTAGCCAGCACTACAGCTAAGGCTATGAGCAAAATGGCTGGATCGAGTGAAGC 633
QY 652 AGCAGAGCCAGGAGGUGUAGUCAGGCUAGGCAAAUGGCUAGGCAAGGCAAGGACCA 711
Db 634 AGCAGAGCCATGGAGGTGTGTAGTCAGGCTAGGCAAAATGGTGCAAGGCGATGAGA 693
QY 712 UGGACUACUCCUAGCUCAGCAGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 771
Db 694 TGGGACTCATCTAGCTCCAGTCTGGTCTGAAAATGCTCTTCTTGAARAATTGCGAGC 753
QY 772 CUUACAGAAACGAUUGGGGUGGCGAGUAGCAACGCUUCAAAGUAGUAGUAGUAGU 824
Db 754 CTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGATCTCTCGCT 806

RESULT 3

PCT-US95-12357A-3
; Sequence 3, Application PC/TUS9512357A
; GENERAL INFORMATION:
; APPLICANT: St. Jude Children's Research Hospital
; TITLE OF INVENTION: Nucleic Acid Encoding Mutant Matrix
; TITLE OF INVENTION: Proteins Useful for Attenuation or Enhancement of
; TITLE OF INVENTION: Influenza A Virus, Vaccines and Methods of making and
; NUMBER OF INVENTIONS: Using Thereof
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/12357A
; FILING DATE: 29-SEPT-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/316,419
; FILING DATE: 30-SEPT-1994
; CLASSIFICATION:
; APPLICATION NUMBER: 08/471,100
; FILING DATE: 6-JUNE-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.048PC01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1027 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Influenza virus
; STRAIN: A/Bangkok/1/79
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 7 (MBANGK)
; PCT-US95-12357A-3

Query Match 73.9%; Score 695.8; DB 6; Length 1027;
Best Local Similarity 73.0%; Pred. No. 2e-157;
Matches 563; Conservative 161; Mismatches 47; Indels 0; Gaps 0;

QY 46 AGAUCUAAAGAGAGAGUCUUAACCGAGGUCGAAACGACGUAUUCUCUUAUCCGUC 105
Db 16 ATATTGAAAGATGAGCCCTTCAACCGAGGTGCGAAGCTATGTTCTCTCTATCGTCCGTC 75
QY 106 AGGCCCCCUAAAGCCGAGAUUGGCAAGAGACUUAAGAGUAGUUCUAGGAGGAACAC 165
Db 76 AGGCCCCCTCAAAGCCGAAATCGCGAGAGACTTGAAGATGTCTTCTGCGAAGAACAC 135
QY 166 CGAUCUUGAGGUUCUUAUGGAUUGGCUAAAGACAAAGCAUUCUUCUACCCUAGCUAA 225
Db 136 AGATCTTTGAGGCTCTCATGGAATGGCTAAAGACAAATCTGTCACTCTGACTAA 195
QY 226 GGGGAUUUAGGUAUUGUGUUCACGCUACCGUCCAGUGAGGAGGAGUAGCAGCGUAG 285
Db 196 GGGGATTTTGGGATTTGTGTTTCAAGCTCACCGTCCCGCCAGTGAGCGAGGAGCTG 255
QY 286 ACGCUUUGUCCAAAUGCCCUUUAUGGGAACGGGGAUCCAAUUAUUAUUAUUAUUAUUA 345
Db 256 ACGCTTTTGTCCAAAATGCCCTCAATGGGAATGGGATCCAAATAAATGAACAGAGCAGT 315
QY 346 UAAACUUAUAGGAAGGCUAAGAGGAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUA 405
Db 316 TAAACTATACAGAAACTTAAGAGGGAGATAACATCTCATGGGCCAAAGAAATAGCACT 375
QY 406 CAGUUAUUCUGCUGGUGCACUUGCCAGUUAUGGCGCUAUAUUAUUAUUAUUAUUAUUA 465
Db 376 CAGTTATTCTGCTGGTGCACCTTGCCAGTTGCATGGGCTCATATACAAACAGGATGG 435
QY 466 UGUGACCAUAGAAUGGCAUUGGCCUGGUAUUGUUAUUAUUAUUAUUAUUAUUAUUA 525
Db 436 TGTAAACCACTGAAGTGGCCCTTGGCCCTGATGTGTGCAACCTGTGTGAACAGATTG 495
QY 526 CCAGCAUCGUCUUAAGGCAAAUGGUGCAACCAACCAACCAACCAACCAACCAACCA 585
Db 496 CCAGCACAGGTCTCTTAGGCAAAATGGTGGCAACCAACCAACCAACCAACCAACCA 555
QY 586 CAGAAUGGUUUUAGCCAGCAUACAGCUAAGGCUAUGGAGCAAAUGGCUAGGAGUAGA 645
Db 556 CAGNATGTTCTGGCCAGCACTACAGCTAAGGCTATGAGCAAAATGGCTGGATCAAGTA 615
QY 646 GCAAGCAGCAGAGCCCAUUGGAGGUUGCUAUGGAGGUUAGGCAAAUGGCUAGGAGUAG 705
Db 616 GCAGGCAGCAGAGGCCATGGAGGTGCTAGTCAGGCCAGGCAAAATGGTGCGAGCAAT 675
QY 706 AACCAUUGGACUUAUCCUAGCUCCAGUCUGGUGAUAUUAUUAUUAUUAUUAUUAUUA 765
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QY 766 GCAGGCCUUAUCAGAAACGAAUUGGGGUGGAGUAGCAACCGGUGUUAUUAUUAUUA 816
Db 736 GCAGACCTATCAGNACAGNATGGGGTGCAGATGCAACGATTCAAGTGACC 786

RESULT 4

US-09-506-286B-1
; Sequence 1, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth

```

; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION: At location 663, r = A or G; At amino acid
; OTHER INFORMATION: location 213, Xaa = Val
US-09-506-286B-1

Query Match      68.7%; Score 647.4; DB 3; Length 1023;
Best Local Similarity 70.8%; Pred. No. 8.1e-146;
Matches 546; Conservative 148; Mismatches 77; Indels 0; Gaps 0;

Qy 46 AGAUCUUAAGAUAGUCUUAACCGAGGUGCAACGUAUCUUCUUAUCCCGUC 105
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Qy 106 AGGCCCCCUAAAGCCGAGATCGCGCAGAGACTTGAAGATGCTTTGCGGGAAGAAC 165
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Qy 166 CGAUCUUGAGUUCUUAUGGAUUGCUAAAGACAAAGCAUCCUGUACCUUAGACUAA 225
Db 135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACCAATCTGTCACTCTGACTAA 194

Qy 226 GGGGAUUUAGAUUUGUUCUACGCUCACCGUGCCAGUGAGCGAGGACUGAGCGUAG 285
Db 195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTCCAGTGGAGGACTGCGAGCGTAG 254

Qy 286 ACGCUUUGCCAAAGUCCUUAUGGAACGGGUAUCCAUUGGGGCCAAAGAAUUCUCACU 345
Db 255 ACGCTTTTCCAAATGCCCTTAGTGGAAACGGAGATCCAAACCAATGCGACAGAG 314

Qy 346 UAAACUGUAAGGAAGCUAAGUGGACAAACCAACCAACCAUUAUACAGACUAGAA 585
Db 315 AAACTGTACAGGAAGCTTAAAGAGAAATAACATTCATGGGCAAAAGAGTGGCACT 374

Qy 406 CAGUUAUUCUGUGUACUAGCGUACUAGCGUAGUAGUAGUAGUAGUAGUAGUAGUAG 465
Db 375 CAGCTATTCCACTGGTGACTAGCGAGCTGATGGGACTATATACACAGAAATGGGAAC 434

Qy 466 UGAGACACUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 525
Db 435 TGTGACAAACCGAAGTGGCATTTGGCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy 526 CCAGCAUCGUGUACUAGUAGGCAAAUGGUGACAAACCAACCAACCAUUAUACAGACUAGAA 585
Db 495 CCAGCATCGATCTCACAGGCAGATGTTGACAAACCAACCAACCAATTAATCAGACATGAAA 554

Qy 586 CAGAAUUGUUUAGCCAGCAUACAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 645
Db 555 CAGAAUUGUUUAGCCAGCAUACAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 614

Qy 646 GCAAGCAGCAGAGGCGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 705
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Qy 706 AACCAUUGGGGACUACUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 765
Db 675 AACCAUUGGGGACUACUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 734

; RESULT 5
US-09-762-861B-1
; Sequence 1, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-09-762-861B-1

Query Match      68.7%; Score 647.4; DB 3; Length 1023;
Best Local Similarity 70.8%; Pred. No. 8.1e-146;
Matches 546; Conservative 148; Mismatches 77; Indels 0; Gaps 0;

Qy 46 AGAUCUUAAGAUAGUCUUAACCGAGGUGCAACGUAUCUUCUUAUCCCGUC 105
Db 15 ATATTTAAGATGATCTTCTGACCGAGTGTGAAATGCTTCTCTATCGTACATC 74

Qy 106 AGGCCCCCUAAAGCCGAGATCGCGCAGAGACTTGAAGATGCTTTGCGGGAAGAAC 165
Db 75 AGGCCCCCTCAAGCCGAGATCGCGCAGAGACTTGAAGATGCTTTGCGGGAAGAAC 134

Qy 166 CGAUCUUGAGUUCUUAUGGAUUGCUAAAGACAAAGCAUCCUGUACCUUAGACUAA 225
Db 135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACCAATCTGTCACTCTGACTAA 194

Qy 226 GGGGAUUUAGAUUUGUUCUACGCUCACCGUGCCAGUGAGCGAGGACUGAGCGUAG 285
Db 195 AGGGATTTTAGGATTCGTATTCACGCTCACCGTCCAGTGGAGGACTGCGAGCGTAG 254

Qy 286 ACGCUUUGCCAAAGUCCUUAUGGAACGGGUAUCCAUUGGGGCCAAAGAAUUCUCACU 345
Db 255 ACGCTTTTCCAAATGCCCTTAGTGGAAACGGAGATCCAAACCAATGCGACAGAG 314

Qy 346 UAAACUGUAAGGAAGCUAAGUGGACAAACCAACCAACCAUUAUACAGACUAGAA 585
Db 315 AAACTGTACAGGAAGCTTAAAGAGAAATAACATTCATGGGCAAAAGAGTGGCACT 374

Qy 406 CAGUUAUUCUGUGUACUAGCGUACUAGCGUAGUAGUAGUAGUAGUAGUAGUAGUAG 465
Db 375 CAGCTATTCCACTGGTGACTAGCGAGCTGATGGGACTATATACACAGAAATGGGAAC 434

Qy 466 UGAGACACUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 525
Db 435 TGTGACAAACCGAAGTGGCATTTGGCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy 526 CCAGCAUCGUGUACUAGUAGGCAAAUGGUGACAAACCAACCAACCAUUAUACAGACUAGAA 585
Db 495 CCAGCATCGATCTCACAGGCAGATGTTGACAAACCAACCAACCAATTAATCAGACATGAAA 554

Qy 586 CAGAAUUGUUUAGCCAGCAUACAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 645
Db 555 CAGAAUUGUUUAGCCAGCAUACAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 614

Qy 646 GCAAGCAGCAGAGGCGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 705
Db 615 GCAGCAGCAGAGGCGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 674

Qy 706 AACCAUUGGGGACUACUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 765
Db 675 AACCAUUGGGGACUACUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 734
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Db 435 TGTGCAACCGAAGTGGCAATTTGGCCCTGGTATGGCCACATGTGAAACAGATCGCTGATTC 494
QY 526 CCAGCAUCGGUCUACAUGGCAAAUUGGUCACAAACCAACCAACCAUUAUCAGACAGAGAA 585
Db 495 CAGCATCGATCTCACAGCAGATGGTGACAAACCAACCAATTAATCAGACATGAAA 554
QY 586 CAGAAUGGUUUUAGCCAGCACUACAGCAAGGCUAUGGAGCAAAUUGGUGGAGUGAGUGA 645
Db 555 CAGAAUGGUUUUAGCCAGCACUACAGCAAGGCUAUGGAGCAAAUUGGUGGAGUGAGUGA 614
QY 646 GCAAGCAGCAGAGGCGCAUGGAGGUUUGUAGUCAGGCUAGGCAAAUUGGUGGAGUGAG 705
Db 615 GCAGGCGCAGAGGCGCAUGGAGGUUUGUAGUCAGGCUAGGCAAAUUGGUGGAGUGAG 674
QY 706 AACCAUUGGGGACUCUACUCCAGUCAGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 765
Db 675 AACCAUUGGGGACUCUACUCCAGUCAGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 734
QY 766 GCAGGCGCAGAGGCGCAUGGAGGUUUGUAGUCAGGCUAGGCAAAUUGGUGGAGUGA 816
Db 735 GCAGGCGCAGAGGCGCAUGGAGGUUUGUAGUCAGGCUAGGCAAAUUGGUGGAGUGA 785

RESULT 6
US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-065-133A-1

Query Match 68.7%; Score 647.4; DB 3; Length 1023;
Best Local Similarity 70.8%; Pred. No. 8.1e-146;
Matches 546; Conservative 148; Mismatches 77; Indels 0; Gaps 0;

QY 46 AGAUCUAAAGAGUGUCUUAACCGAGGUGGAGAAACGUACUGUCUUAUCUUAUCCCGUC 105
Db 15 ATATTTAAAGATGAGTCTTCTGACCGAGGTGCAACGACGTCTCTCTATCGTACCATC 74
QY 106 AGGCCCCCUAAGCCGAGAGUAGCAGAGACUUAUGAUGUUAUGGAGGAGAAACAC 165
Db 75 AGGCCCCCTCAAGCCGAGATCGGCGAGAGATTTGAAGATGCTTTGCGAGGAGAAACAC 134
QY 166 CGAUCUAGGAGUUCUUAUGGAGUAGGCUAAGCAAGCAACCAUCCUGUACCCUUGACUAA 225
Db 135 CGATCTTGAGGACCTCATGGAATGGCTTAAGACAAACCAATCTGTCACTCTGACTTAA 194
QY 226 GGGGAUUUUAAGGAUUUGUUGUUCACGUCACCGUGGCCAGUGAGGAGGAGGAGCGGUGAG 285

Db 195 AGGGAATTTAGGATTCGTATTACCGCTCACCGTCCCGCAGTGAGCGAGGACTGCGACGTAG 254
QY 286 ACGUUUGUCCAAAUUGCCCUUAUUGGGAACGGGGAUCCAAUAAACAUAGGACAAAGCAGU 345
Db 255 AGCTTTGTCCAAATAGCCCTTGTAGTGAACGGAGATCCAAACNACATGACAGACGAGT 314
QY 346 UAAACUGUUAAGGAAGCUCAGAGGGAGAAUUAUCCUUGGGGCCAAAGAAAUUCACU 405
Db 315 AAAACTGTACAGGAAGCTTAAAGAGAGAAATAACATTCATGGGGCAAAAGAGGTGGCACT 374
QY 406 CAGUUUUAUUGGUGGUGCAGUUGCCAGUUAUUGGGGCUUAUUAACACAGGAUUGGGGC 465
Db 375 CAGCTATTCCACTGGTGCACCTAGCCAGCTGACATGGGACTCATATACACAGAAATGGGAAC 434
QY 466 UGUGACACUAGUAGGUGGCUUUGGCCUGGUAUUGCAACUGGAGAAACAGAUUGUGUAGUC 525
Db 435 TGTGACAAACGAGTGGCATTTGGCCCTGGTATGGCCACATGTGGAACAGATCGCTGATTC 494
QY 526 CCAGCAUCGGUCUACAUGGCAAAUUGGUGACAAACCAACCAACCAUUAUCAGACAGAA 585
Db 495 CCAGCATCGATCTCACAGGCGAGATGGTGACAAACCAACCAACCAATTAATCAGACATGAAA 554
QY 586 CAGAAUGGUUUUAGCCAGCACUACAGCAAGGCUAUGGAGCAAAUUGGAGGAGUAGUGA 645
Db 555 CAGAAUGGUUUUAGCCAGCACUACAGCAAGGCUAUGGAGCAAAUUGGAGGAGUAGUGA 614
QY 646 GCAAGCAGCAGAGGCGCAUGGAGGUUUGUAGUCAGGCUAGGCAAAUUGGUGGAGUGAG 705
Db 615 GCAGGCGCAGAGGCGCAUGGAGGUUUGUAGUCAGGCUAGGCAAAUUGGUGGAGUGAG 674
QY 706 AACCAUUGGGGACUCUACUCCAGUCAGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 765
Db 675 AACCAUUGGGGACUCUACUCCAGUCAGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 734
QY 766 GCAGGCGCAGAGGCGCAUGGAGGUUUGUAGUCAGGCUAGGCAAAUUGGAGGAGUAG 816
Db 735 GCAGGCGCAGAGGCGCAUGGAGGUUUGUAGUCAGGCUAGGCAAAUUGGAGGAGUAG 785

RESULT 7
US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (663)..(663)
; OTHER INFORMATION: At nucleotide 663, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-434-811A-1

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Query Match      68.7%; Score 647.4; DB 3; Length 1023;
Best Local Similarity 70.8%; Pred. No. 8.1e-146;
Matches 546; Conservative 148; Mismatches 77; Indels 0; Gaps 0;

Qy 46 AGAUCUAAAGAGUUCUUAACCGAGGUGGAAACGUAUCUUCUUAUCCGUC 105
Db 15 ATATTTAAAGATGAGTCTTCTGACCGAGGTGCGAAGCTGCTCTCTATCTGACATC 74

Qy 106 AGGCCCCCUAAAGCGAGUUCGACAGAGACUUAAGAUUGUUGCAGGGAAGACAC 165
Db 75 AGGCCCCCTCAAGCGAGATCGCGCAGAGACTTGAAGATGCTTTGCGAGGAAGAACAC 134

Qy 166 CGAUUCUAGGUUCUUAAGGUAAGGCUAAGACAGACAGACUUAAGAUUGUUGCAGGUA 225
Db 135 CGATCTTGAGGCACTCATGGAATGGCTTAAGACAGACCAATCTGTCACTCTGACTAA 194

Qy 226 GGGGAUUAAGGUUCUUAAGGUAAGGCUAAGACAGACAGGAGGAGGAGGAGG 285
Db 195 AGGATTTTAGGATTCGATTCACGCTCACCCTGCCAGTGGAGGAGCTGCGAGCTAG 254

Qy 286 ACGCUUUGUCCAAAUUGCCCUUAUUGGGAACGGGGAUCCAAUUAACAUAGCAAGCAGU 345
Db 255 ACGCTTTGTCCAAATGCCCTTAGTGGAAACGGAGATCCAAACCAACATGGACAGCAGT 314

Qy 346 UAAACUUAUAGGAGUUCUUAAGGUAAGGCUAAGACAGACAGGAGGAGGAGG 405
Db 315 AAAAAGTGTACAGGAAGCTTAAAGAGAAATAAATTCATCGGCGCAAAAGAGGTGGCACT 374

Qy 406 CAGUUAUUCUGCUGGAGUUCUUAAGGUAAGGCUAAGACAGGAGGAGGAGGAGG 465
Db 375 CAGCTATTCACCTGGTGCATAGCCAGCTGATGGACTCATATACACAGATGGGAAAC 434

Qy 466 UGAGACCAUGAAGUUGCAUUGGCUUUGGUAAGUUGCAACUUGGUAAGUUGCAGUC 525
Db 435 TGTGACAAACCGAAGTGGCAATTTGGCTGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy 526 CCAGCAUUGGCUUUAAGGUAAGGCUUUAAGGUAAGGCUUUAAGGUAAGGUAAG 585
Db 495 CCAGCATCGATCTCAGAGGAGCTTAAAGAGAAATAAATTCATCGGCGCAAAAGAGGTGGCACT 554

Qy 586 CAGAAUUGGUUUAAGGCUUUAAGGUAAGGCUUUAAGGUAAGGCUUUAAGGUAAG 645
Db 555 CAGATGTGATTTAGCCAGTACACCGCTTAAGCCATGGAGCAGATGGCAGGCTCGATGA 614

Qy 646 GCAAGCAGCAGAGGCUUUAAGGUAAGGCUUUAAGGUAAGGCUUUAAGGUAAG 705
Db 615 GCAGGACAGAGGCGCATGGAGGTGCTAGTAAAGCTAGGCAAGATGGTRCAGGCAATGAG 674

Qy 706 AACCAUUGGAGUUCUUAAGGUAAGGCUUUAAGGUAAGGCUUUAAGGUAAG 765
Db 675 AACCATTTGGGACCCACCTAGCTCCAGTGGCGGTTTGAAGATGATCTCTTGAATAATTT 734

Qy 766 GCAGGCUUUAAGGUAAGGCUUUAAGGUAAGGCUUUAAGGUAAGGCUUUAAGGUAAG 816
Db 735 GCAGGCTTACCAGAAACGGATGGGAGTGCATAATGCAGCGCATTCAGATGATC 785
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RESULT 8
US-09-506-286B-4
; Sequence 4, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506, 286B
; PENDING FILING DATE: 2000-02-16
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
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; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25) .. (780)
US-09-506-286B-4

Query Match      68.4%; Score 644.6; DB 3; Length 1023;
Best Local Similarity 70.7%; Pred. No. 3.8e-145;
Matches 545; Conservative 147; Mismatches 79; Indels 0; Gaps 0;

Qy 46 AGAUCUAAAGAGUUCUUAACCGAGGUGGAAACGUAUCUUCUUAUCCGUC 105
Db 15 ATATTTAAAGATGAGTCTTCTGACCGAGGTGCGAAGCTGCTCTCTATCTTACCATC 74

Qy 106 AGGCCCCCUAAAGCGAGUUCGACAGACAGACUUAAGAUUGUUGCAGGGAAGACAC 165
Db 75 AGGCCCCCTCAAGCGAGATCGCGCAGAGACTTGAAGATGCTTTGCGAGGAAGAACAC 134

Qy 166 CGAUUCUAGGUUCUUAAGGUAAGGCUAAGACAGACAGACUUAAGAUUGUUGCAGGUA 225
Db 135 CGATCTTGAGGCACTCATGGAATGGCTTAAGACAGACCAATCTGTCACTCTGACTAA 194

Qy 226 GGGGAUUAAGGUUCUUAAGGUAAGGCUAAGACAGACAGGAGGAGGAGGAGG 285
Db 195 AGGATTTTAGGATTCGATTCACGCTCACCCTGCCAGTGGAGGAGCTGCGAGCTAG 254

Qy 286 ACGCUUUGUCCAAAUUGCCCUUAUUGGGAACGGGGAUCCAAUUAACAUAGCAAGCAGU 345
Db 255 ACGCTTTGTCCAAATGCCCTTAGTGGAAACGGAGATCCAAACCAACATGGACAGCAGT 314

Qy 346 UAAACUUAUAGGAGUUCUUAAGGUAAGGCUAAGACAGACAGGAGGAGGAGG 405
Db 315 AAAAAGTGTACAGGAAGCTTAAAGAGAAATAAATTCATCGGCGCAAAAGAGGTGGCACT 374

Qy 406 CAGUUAUUCUGCUGGAGUUCUUAAGGUAAGGCUUUAAGGUAAGGCUUUAAGGUAAG 465
Db 375 CAGCTATTCACCTGGTGCATAGCCAGCTGATGGACTCATATACACAGATGGGAAAC 434

Qy 466 UGAGACCAUGAAGUUGCAUUGGCUUUGGUAAGUUGCAACUUGGUAAGUUGCAGUC 525
Db 435 TGTGACAAACCGAAGTGGCAATTTGGCTGTATGCGCCACATGTGAACAGATCGCTGATTC 494

Qy 526 CCAGCAUUGGCUUUAAGGUAAGGCUUUAAGGUAAGGCUUUAAGGUAAGGUAAG 585
Db 495 CCAGCATCGATCTCAGAGGAGCTTAAAGAGAAATAAATTCATCGGCGCAAAAGAGGTGGCACT 554

Qy 586 CAGAAUUGGUUUAAGGCUUUAAGGUAAGGCUUUAAGGUAAGGCUUUAAGGUAAG 645
Db 555 CAGATGTGATTTAGCCAGTACACCGCTTAAGCCATGGAGCAGATGGCAGGCTCGATGA 614

Qy 646 GCAAGCAGCAGAGGCUUUAAGGUAAGGCUUUAAGGUAAGGCUUUAAGGUAAG 705
Db 615 GCAGGACAGAGGCGCATGGAGGTGCTAGTAAAGCTAGGCAAGATGGTRCAGGCAATGAG 674

Qy 706 AACCAUUGGAGUUCUUAAGGUAAGGCUUUAAGGUAAGGCUUUAAGGUAAG 765
Db 675 AACCATTTGGGACCCACCTAGCTCCAGTGGCGGTTTGAAGATGATCTCTTGAATAATTT 734

Qy 766 GCAGGCUUUAAGGUAAGGCUUUAAGGUAAGGCUUUAAGGUAAGGCUUUAAGGUAAG 816
Db 735 GCAGGCTTACCAGAAACGGATGGGAGTGCATAATGCAGCGCATTCAGATGATC 785

RESULT 9
US-09-762-861B-4
; Sequence 4, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
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Q7

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Db 495 CCAGCATCGATCTCACAGGCAGATGGTGCACATTAACCAACCCATTAATCAGACATGAAA 554
Qy 586 CAGAAUGUUUAGCCAGACACUACAGCUGUAAGGCUAGGCAAAUUGGCUUGGAGUGA 645
Db 555 CAGAAUGUUUAGCCAGACACUACAGCUGUAAGGCUAGGCAAAUUGGCUUGGAGUGA 614
Qy 646 GCAAGCAGCAGAGCCAGGAGGUGUUGUAGCAGGCUAGGCAAAUUGGCUUGGAGUGA 705
Db 615 GCAGGCAGCAGAGCCAGGAGGUGUUGUAGCAGGCUAGGCAAAUUGGCUUGGAGUGA 674
Qy 706 AACCAUUGGAGACUACUAGCUCAGGUGGUGUUGUAGGCAAAUUGGCUUGGAGUGA 765
Db 675 AACCAUUGGAGACUACUAGCUCAGGUGGUGUUGUAGGCAAAUUGGCUUGGAGUGA 734
Qy 766 GCAGGCACUACAGAAACGAAUUGGUGGUGGUGGAGUAGCAACCGGUCUAGGAGAAC 816
Db 735 GCAGGCCTACAGAAACGGAATGGAGTGGAGTGCACCAATGCAGGATTCAGATGATC 785

RESULT 11
US-10-434-811A-4
; Sequence 4, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-CL-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
US-10-434-811A-4

Query Match 68.4%; Score 644.6; DB 3; Length 1023;
Best Local Similarity 70.7%; Pred. No. 3.8e-145;
Matches 545; Conservative 147; Mismatches 79; Indels 0; Gaps 0;

Qy 46 AGAUCUAAAGAGAGUUCUUAACCGAGGUGGAAACGUCUUCUUCUUAUCUUCGUC 105
Db 15 ATATTTAAGATGATCTTTCACGAGGATCGAAACGATCTTCTCTATCTTACCATC 74

Qy 106 AGGCCCCCUCAAGCCGAGUAGCGCAGAGACUUGAAGUUCUUGCAGGGAAGAACAC 165
Db 75 AGGCCCCCTCAAGCCGAGATCGCGCAGAGACTTGAAGATGCTTTTGCAGGGAAGAACAC 134

Qy 166 CGAUCUUGAGUUCUUAUGGAUAGGCUAAGACAGACCAUUCUUGCAGGCUUACUUA 225
Db 135 CGATCTTGAGGCACTCATGGAATGGCTAAAGACAGACCAATCTCTGTCACCTCTGACTAA 194

Qy 226 GGGGAUUUAGGAUUUGUUCUACGUCACCGUGCCAGUGAGGAGGAGGAGGAGCGGUG 285
Db 195 AGGGATTTAGATTCGTATTCACCTCACCGTCCCGAGTGAAGGAGCTGACGCGTAG 254

Qy 286 ACGCUUUGUCCAAUUGCCUUUAUUGGGAACGGGGAUCCAAUUAACAUUGGACAGU 345
Db 255 ACGCTTTGTCAAAATGCCCTTAGTGGAAACCGAGATCCAAACCAACATGGGACAGCAGT 314

Qy 346 UAAACUGUUAAGGAGGCUAAGAGGAGGAGAAUACAUUCCUAGGCGGCAAGAAUUCUACU 405
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Db 315 AAAAATGTACAGGAAGCTTAAAGAGAAATAACATTCATGGGCAAAAGAGGTGGCACT 374
Qy 406 CAGUUAUUCUGUGGUGCACAUCUGCCAGUUGUUAUGGCGCUCAUUAACAACAGGAUGGGGC 465
Db 375 CAGCTATTCCACTGGTGTGCTAGCCAGCTGCTAGGGACTCATATACACAGAATGGGAAC 434
Qy 466 UGUGACCAUAGAAGUGGCAUUGGCGUUGUUGGCAACCGUGAAGCAGAUUUGCAGUC 525
Db 435 TGTGACAAACGAAAGTGGCATTTTGGCTGTATGCGCCACATGTGGAACAGATCGCTGATTC 494
Qy 526 CCAGCAUCGUGUCUUAAGGCAAAUUGGCAACCAACCAACCCACAAUUAACAGACAUGA 585
Db 495 CCAGCATCGATCTCACAGGCAGATGGTGCACATTAACCAACCCATTAATCAGACATGAAA 554
Qy 586 CAGAAUGUUUAGCCAGACACUACAGCUGUAAGGCUAGGCAAAUUGGCUUGGAGUGA 645
Db 555 CAGAAUGUUUAGCCAGACACUACAGCUGUAAGGCUAGGCAAAUUGGCUUGGAGUGA 614
Qy 646 GCAAGCAGCAGAGCCAGGAGGUGUUGUAGCAGGCUAGGCAAAUUGGCUUGGAGUGA 705
Db 615 GCAGGCAGCAGAGCCAGGAGGUGUUGUAGCAGGCUAGGCAAAUUGGCUUGGAGUGA 674
Qy 706 AACCAUUGGAGACUACUAGCUCAGGUGGUGUUGUAGGCAAAUUGGCUUGGAGUGA 765
Db 675 AACCAUUGGAGACUACUAGCUCAGGUGGUGUUGUAGGCAAAUUGGCUUGGAGUGA 734
Qy 766 GCAGGCACUACAGAAACGAAUUGGUGGUGGUGGAGUAGCAACCGGUCUAGGAGAAC 816
Db 735 GCAGGCCTACAGAAACGGAATGGAGTGGAGTGCACCAATGCAGGATTCAGATGATC 785

RESULT 12
US-09-506-286B-3
; Sequence 3, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-3

Query Match 67.6%; Score 637.2; DB 3; Length 756;
Best Local Similarity 71.0%; Pred. No. 2.1e-143;
Matches 537; Conservative 145; Mismatches 74; Indels 0; Gaps 0;

Qy 56 AUGAGUUCUUAACCGAGGUGGAAACGUAUCUUCUUAUCUUAUCUUCAGGCGCCUC 115
Db 1 ATGAGTCTTCTGACCGAGGTCGAAACGATCGTCTCTATCTGTACCATCAGGCCCCCTC 60

Qy 116 AAAGCCGAGAUCCGACAGACUUGAAGUUGUUGUAGGAGGAGGAGGAGGAGGAGG 175
Db 61 AAAGCCGAGATCGGACAGACTTGAAGATGCTTTTCAGGGAAGAACACCGATCTTGAG 120

Qy 176 GUUCUUAUGGAUUGGCUUUAAGACAGACCAUUCUUGUACCUUGCAGUAGGGAUUA 235
Db 121 GCATCATGAATGGCTTAAAGACAGACCAATCTGTCTGTCTGTCTGTCTGTCTGTCT 180

Qy 236 GGAUUUGUUCAGGUCUACCGGUGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 295
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Db 181 GGAATTCGATTATTCACCGTCCACCGTGCAGTGCAGGAGACTGCAGCGTAGACGCTTTGTC 240
Qy 296 CAAAUAUGCCUUAUUGGGAACCGGGAUCCAAUAUACUGGCAAGCAGUUAACUGUUAU 355
Db 241 CAAAATGCCCTTAGTGGGAACCGGAGATCCAAACAACTGGACAGAGCATGTAAGACTGTAC 300
Qy 356 AGGAAGCUCUAGAGGAGGAGUAAACAUUCCAUUGGGGCCAAAGAAUUCUCACUCAGUUAUUCU 415
Db 301 AGGAAGCTTTAAAGAGAGAAATTAACATTCATGGGGCAAAAGAGGTGGCACTCAGCTATTCC 360
Qy 416 GCUGUGCACAUCUGCAGUUAUUGGCCUUAUUAUACAAACAGAGUUGGGGCGUGUAGCCACU 475
Db 361 ACTGCTGCACTAGCCAGCTGCACTGGAATCATATACACAGAACTGGGAACCTGTGACAAAC 420
Qy 476 GAAUGGCAUUGGCCUUGGUAUGGCAACUGGCAACAGUUAUUGGCAUUGGCCAGCAUGGG 535
Db 421 GAAGTGGCATTTGGGCTGGTATGGCCACATGTGAACAGATCGCTGATTTCCAGCATCGA 480
Qy 536 UCUAUAGGCAAAUGGUGACAAACCAACCAACCAUUAUCAGACAUAGAAACAGAAUGGU 595
Db 481 TCTCAGCGCAGATGCTGACAAACCAACCAACCATTAATCAGACATGAAACAGAAATGGTA 540
Qy 596 UUAGCCAGCACAUAAGCAGUUAUGGCAAAUUGGCGUUAUUGGCAAGCAAGCAAGCA 655
Db 541 TTAGCCAGTACCAACCGCTAAAGCCATGGAGCAGATGGCAGGCTCGAGTGAGCAGCAGCA 600
Qy 656 GAGGCCAUGGAGGUUGUAGUCAGGCUAGGCAAGCAAAUUGGCAAGCAAGCAACCAUUGG 715
Db 601 GAGGCCATGGAGGTTGGTAGTAAGGCTAGGAGCAGATGGTTCAGGCAATGAGAAACCATGGG 660
Qy 716 ACUAUCCUAGCUCAGUUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 775
Db 661 ACCACCTAGCTCAGTCCGCGTTTGAAGATGATCTCTTGAATTTGCGAGGCTTAC 720
Qy 776 CAGAAACGAUUGGGGUGCAGAUAGCAACCGUUAAG 811
Db 721 CAGAAACGGATGGAGTGCAAAATGCAGCGATTCAAG 756

RESULT 13

US-09-762-861B-3
; Sequence 3, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-762-861B-3

Query Match 67.6%; Score 637.2; DB 3; Length 756;
Best Local Similarity 71.0%; Pred. No. 2.1e-143;
Matches 537; Conservative 145; Mismatches 74; Indels 0; Gaps 0;
Qy 56 AUGAGUCUUAUACCGAGGUGGAAACGUAUGUUCUUAUUGGUGGUGGUGGUGGUGGUGG 115
Db 1 ATGAGTCTTCTGACCGAGGTGCAAAACGTAACGTTCTCTATCGTACCATCATGAGGCCCTC 60

Qy 116 AAAGCCGAGUACGACAGAGACUUGAAGAUUGUUCUUGCAGGGAAGAACACCGAUUCUGAG 175
Db 61 AAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGACGGAAGAACACCGATCTTGAG 120
Qy 176 GUUUCUAUGAUGGCUAAAGACAGACCAACUCCUGUACCUUGACUUAAGGGAUUUA 235
Db 121 GCACTCATGAATGGCTTAAAGACAAGACCAATCTCTGTCTGACTAAGGGATTTTA 180
Qy 236 GGAUUGUGUUCAGCUCACCGUCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 295
Db 181 GGATTCGATTTACGCTCAGCGTCCGAGTGGAGGAGGAGTGCAGCGTAGACGCTTTGTC 240
Qy 296 CAAAUAUGCCUUAUUGGGAACCGGGAUCCAAUAUACAGCAAAAGCAGUUAACUGUUA 355
Db 241 CAAAATGCCCTTAGTGGAAACCGGAGATCCAAACAACTGACAGAGCAGTAAAACTGTAC 300
Qy 356 AGGAGCUCUAGAGGAGGAGUAAACAUUCCAUUGGGGCCAAAGAAUUCACUCAGUUAUUCU 415
Db 301 AGGAAGCTTTAAAGAGAGAAATAACATTCATGGGGCAAAAGAGGTGGCACTCAGCTATTCC 360
Qy 416 GCUGUGCACAUCUGCAGUUAUUGGGCCUUAUUAUACAAACAGGAGUGGGGUGUAGCCACU 475
Db 361 ACTGCTGCACTAGCCAGCTGCATGGGACTCATATACAAAGATGGGAACCTGTGACAAAC 420
Qy 476 GAAUGGCAUUGGCCUUGGUAUGGCAACCGUUGAAGCAGAUUGGUGGUGGUGGUGGUGG 535
Db 421 GAAGTGGCATTTGGCCTGGTATGGCCACATGTGAACAGATCGCTGATTTCCAGCATCGA 480
Qy 536 UCUAUAGGCAAAUGGUGACAAACCAACCAACCAUUAUCAGACAUAGAAACAGAAUGGU 595
Db 481 TCTCAGCGCAGATGCTGACAAACCAACCAACCATTAATCAGACATGAAACAGAAATGGTA 540
Qy 596 UUAGCCAGCACAUAAGCAGUUAUGGCAAAUUGGCGUUAUUGGCAAGCAAGCAAGCA 655
Db 541 TTAGCCAGTACCAACCGCTAAAGCCATGGAGCAGATGGCAGGCTCGAGTGAGCAGCAGCA 600
Qy 656 GAGGCCAUGGAGGUUGUAGUAGGCUAGGCAAGCAAAUUGGCAAGCAAGCAACCAUUGG 715
Db 601 GAGGCCATGGAGGTTGCTAGTAAGGCTAGGAGCAGATGGTTCAGGCAATGAGAAACCATGGG 660
Qy 716 ACUAUCCUAGCUCAGUUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 775
Db 661 ACCACCTAGCTCAGTCCGCGTTTGAAGATGATCTCTTGAATTTGCGAGGCTTAC 720
Qy 776 CAGAAACGAUUGGGGUGCAGAUAGCAACCGUUAAG 811
Db 721 CAGAAACGGATGGAGTGCAAAATGCAGCGATTCAAG 756

RESULT 14

US-10-065-133A-3
; Sequence 3, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-3

Query Match 67.6%; Score 637.2; DB 3; Length 756;

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2006, 23:29:50 ; Search time 925.936 Seconds
(without alignments)
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Title: US-10-729-830-5

Perfect score: 942

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications NA Main:
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	942	100.0	942	8	US-10-729-830-5	Sequence 5, Appli
2	774	82.2	774	8	US-10-729-830-1	Sequence 1, Appli
3	764.6	81.2	1027	6	US-10-177-390-31	Sequence 31, Appl
4	761.4	80.8	1027	6	US-10-855-875-5	Sequence 5, Appli
5	718.2	76.2	1027	7	US-10-381-530-7	Sequence 7, Appli
6	666.8	70.8	942	8	US-10-729-830-6	Sequence 6, Appli
7	655.4	69.6	986	8	US-10-866-484-9	Sequence 9, Appli
8	647.4	68.7	1023	6	US-10-065-133A-1	Sequence 1, Appli
9	647.4	68.7	1023	6	US-10-434-811A-1	Sequence 1, Appli
10	647.4	68.7	1023	7	US-10-734-373-1	Sequence 1, Appli
11	647.4	68.7	1023	8	US-10-872-014-1	Sequence 1, Appli
12	645.8	68.6	1002	3	US-09-747-335-3	Sequence 3, Appli
13	645.8	68.6	1002	7	US-10-435-723A-3	Sequence 3, Appli
14	644.6	68.4	1023	6	US-10-065-133A-4	Sequence 4, Appli
15	644.6	68.4	1023	7	US-10-434-811A-4	Sequence 4, Appli
16	644.6	68.4	1023	7	US-10-734-373-4	Sequence 4, Appli
17	644.6	68.4	1023	8	US-10-872-014-4	Sequence 4, Appli
18	637.2	67.6	756	6	US-10-065-133A-3	Sequence 3, Appli
19	637.2	67.6	756	7	US-10-434-811A-3	Sequence 3, Appli
20	637.2	67.6	756	7	US-10-734-373-3	Sequence 3, Appli
21	637.2	67.6	756	8	US-10-872-014-3	Sequence 3, Appli
22	634.4	67.3	756	6	US-10-065-133A-6	Sequence 6, Appli
23	634.4	67.3	756	7	US-10-434-811A-6	Sequence 6, Appli

24	634.4	67.3	756	7	US-10-734-373-6	Sequence 6, Appli
25	634.4	67.3	756	8	US-10-872-014-6	Sequence 6, Appli
26	632.6	67.2	816	6	US-10-371-525-13	Sequence 13, Appl
27	632.6	67.2	816	6	US-10-371-069-13	Sequence 13, Appl
28	632.6	67.2	816	6	US-10-371-645-13	Sequence 13, Appl
29	632.6	67.2	816	6	US-10-371-260-13	Sequence 13, Appl
30	627.8	66.6	759	8	US-10-617-569-3	Sequence 3, Appli
31	608.8	64.6	1011	8	US-10-729-830-7	Sequence 7, Appli
32	499.8	53.1	775	8	US-10-729-830-3	Sequence 3, Appli
33	486.8	51.7	844	8	US-10-729-830-4	Sequence 4, Appli
34	99.6	10.6	132	3	US-09-835-694-54	Sequence 54, Appl
35	96.6	10.3	129	3	US-09-835-694-55	Sequence 55, Appl
36	87.4	9.3	122	3	US-09-835-694-17	Sequence 17, Appl
37	84.2	8.9	573	7	US-10-424-599-135848	Sequence 135848,
38	83.4	8.9	362	8	US-10-425-115-68338	Sequence 68338, A
39	83	8.8	598	7	US-10-021-323-11423	Sequence 11423, A
40	82.8	8.8	510	7	US-10-437-963-1928	Sequence 1928, Ap
41	82.6	8.8	374	7	US-10-437-963-32121	Sequence 32121, A
42	82	8.7	405	8	US-10-425-115-76344	Sequence 76344, A
43	82	8.7	1714	8	US-10-425-115-170894	Sequence 170894,
44	81.6	8.7	554	7	US-10-021-323-4489	Sequence 4489, Ap
45	81.6	8.7	559	7	US-10-021-323-14094	Sequence 14094, A

ALIGNMENTS

RESULT 1

US-10-729-830-5
; Sequence 5, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/BP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 942
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA with stabilisation sequences
; FEATURE:
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
; OTHER INFORMATION: respectively.
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
; OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-5

Query Match 100.0%; Score 942; DB 8; Length 942;
Best Local Similarity 100.0%; Pred. No. 1.8e+220;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GCUUUUUUUUUUGCAGAAGCUCAGAAUAAACGCUAACUUUUGCGAGAUAAAGUAG 60
Db	1	GCUUUUUUUUUUGCAGAAGCUCAGAAUAAACGCUAACUUUUGCGAGAUAAAGUAG 60
Qy	61	UCUUUUAACCGAGGUCGAAACGUAAGUUCUCUAUACUCCGUCAGGCCCCCUCAAGC 120
Db	61	UCUUUUAACCGAGGUCGAAACGUAAGUUCUCUAUACUCCGUCAGGCCCCCUCAAGC 120
Qy	121	CGAGUCCGACAGACUUGAAGUUGUUUGCGAGGAAGAACACCGAUUCUUGAGGUUCU 180

Db 121 CGAUCGACAGAGACUUGAAGAUUGUUUGAGGAGAACACCGAUUUUGAGGUUCU 180
Qy 181 CAUGGAAUUGGUAAGAGCAAGACCAUCCUGUCACCUUGACUAAAGGGGUAUUUAGGAU 240
Db 181 CAUGGAAUUGGUAAGAGCAAGACCAUCCUGUCACCUUGACUAAAGGGGUAUUUAGGAU 240
Qy 241 UGUGUUCACGUCUACCGUGGCCAGUGAGCGAGGAGCUGCAGGCUAGAGCGUUUGUCCAAAA 300
Db 241 UGUGUUCACGUCUACCGUGGCCAGUGAGCGAGGAGCUGCAGGCUAGAGCGUUUGUCCAAAA 300
Qy 301 UGCCUUUAUUGGGAACGGGAUCCAAUAUAUCGACCAAAAGCAGUUAACUGUAAGGAA 360
Db 301 UGCCUUUAUUGGGAACGGGAUCCAAUAUAUCGACCAAAAGCAGUUAACUGUAAGGAA 360
Qy 361 GCUCAAGAGGAGAGAAUACAUUCCUAGUGGGCCAAAGAAUUCACUCAGUUAUUCUGUGG 420
Db 361 GCUCAAGAGGAGAGAAUACAUUCCUAGUGGGCCAAAGAAUUCACUCAGUUAUUCUGUGG 420
Qy 421 UGCAUUGCCAGUUGUAUUGGCGCUUAUAUAACAAGAGUUGGGGCGUGUAGCACUGAAGU 480
Db 421 UGCAUUGCCAGUUGUAUUGGCGCUUAUAUAACAAGAGUUGGGGCGUGUAGCACUGAAGU 480
Qy 481 GGCATUUGCCUGUUAUGCAACUUGUAGACAGUUGUCUACUCCAGCAUCCGUCUCA 540
Db 481 GGCATUUGCCUGUUAUGCAACUUGUAGACAGUUGUCUACUCCAGCAUCCGUCUCA 540
Qy 541 UAGGCAAAUUGGUGACAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 600
Db 541 UAGGCAAAUUGGUGACAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 600
Qy 601 CAGCAUACAGCUAAGGCUAUGGAGCAAAUUGGUGUAGUAGGAGCAAGCAGCAGAGGC 660
Db 601 CAGCAUACAGCUAAGGCUAUGGAGCAAAUUGGUGUAGUAGGAGCAAGCAGCAGAGGC 660
Qy 661 CAUGGAGUUGCUAGUCAGGCUAGGCAAAUUGGUGUAGUAGGAGCAAGCAGCAGAGGC 720
Db 661 CAUGGAGUUGCUAGUCAGGCUAGGCAAAUUGGUGUAGUAGGAGCAAGCAGCAGAGGC 720
Qy 721 UCCUAGCUCCAGUGUGUGUUGAAAAUUGAUUUUUUGAAAAUUUGAGGCGCUAUCAGAA 780
Db 721 UCCUAGCUCCAGUGUGUGUUGAAAAUUGAUUUUUUGAAAAUUUGAGGCGCUAUCAGAA 780
Qy 781 ACAGAAUGGGGUGCAGAGUACCGUUAAGUUAACUAGUAGUAGUAGUAGGCGCGUGGCG 840
Db 781 ACAGAAUGGGGUGCAGAGUACCGUUAAGUUAACUAGUAGUAGUAGUAGGCGCGUGGCG 840
Qy 841 CUCCCAAGGGCGCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCC 900
Db 841 CUCCCAAGGGCGCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCC 900
Qy 901 AA 942
Db 901 AA 942

RESULT 2
US-10-729-830-1
; Sequence 1, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Influenza virus
; FEATURE:
; OTHER INFORMATION: Influenza matrix: wildtype gene (for comparison)
; FEATURE:
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
; OTHER INFORMATION: codon: tga (nucleotides 767 to 769)
US-10-729-830-1

Query Match 82.2%; Score 774; DB 8; Length 774;
Best Local Similarity 77.6%; Pred. No. 2.4e-179;
Matches 601; Conservative 173; Mismatches 0; Indels 0; Gaps 0;

Qy 46 AGAUUUUAAGAGAGAGUUCUUAACCGAGGUCGAAACGUAUUCUUCUUAUUAUUAUUAU 105
Db 1 AGATCTAAAGATGAGTCTTCTAACCGAGGTCGAAACGTCAGTCTCTCTATCATCCGCTC 60
Qy 106 AGGCCCCCUCAAGCCGAGAUCCGACAGACAUUUGAAGAUUGUUUGCAGGGAAGACAC 165
Db 61 AGGCCCCCTCNAAGCCGAGATCGACAGAGCTTGAAGATGTCTTTGACGGGGAAGACAC 120
Qy 166 CGAUUUUAGGUCUUAUGGAUUGGCUAAGACAAAGACAAUCCUGUCACCUUCUGACUAA 225
Db 121 CGATCTTGAGGTCTCTATGGAATGGCTAAAGACAGACCAATCTGTCACTCTGACTAA 180
Qy 226 GGGGAUUUAAGGAUUUGUUCACGUCACCGUCCGAGGCGGAGGACUGCAGCGUAG 285
Db 181 GGGGATTTTAGGATTTGTGTTCACTGCTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGTCC 240
Qy 286 ACGUUUUGCCAAAUUGCCCUUAUUGGGAACGGGGAUUAUUAUUAUUAUUAUUAUUAUUA 345
Db 241 ACGCTTTGTCCAAATGCCCCCTTAATGGGAACGGGGATCCAAATTAACATGCAAGAGCGT 300
Qy 346 UAAACUUGUUAAGGAAGCUCAAAGAGGAGUAAUAUUAUUAUUGGGGCCAAAGAAUUCACU 405
Db 301 TAAACTGTATAGAGAGCTCAAGAGGGAGATTAATTCATTCATGGGGCCAAAGAAATCTCA 360
Qy 406 CAGUUAUUCUGUGGUGUACUUGCCAGUUGUUAUUGGGCCUUAUAUAACAGGAGGCGGC 465
Db 361 CAGTTATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Qy 466 UGUGACCAUAGAGGCAUUGGCGUUAUUGGCGUUAUUGGCAACCUUGAAGCAGAUUGCUGAC 525
Db 421 TGTGACCACTGAAAGTGGCAATTTGGCTGGTATGTGTGCAACCTGTGAAACAGATTGCTGAC 480
Qy 526 CCAGUACUGGUCUUAUAGGCAAAUUGGUGACAAACCAACCAACCAACCAACCAACCAACCA 585
Db 481 CCAGCATCGGTCTCATAGGCAAAATGGTGACAAACCAACCAACCAACCAACCAACCAACCA 540
Qy 586 CAGAAUUGGUUUUAGCCAGACUACAGCUAAGGCUAUGGAGCAAAUUGGCGUUAUUGGAGUGA 645
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Qy 646 GCAAGCAGCAGAGCCCAUGGAGGUGUUAUUGGCGUUAUUGGCAACCUUGGCAAGGAGUAG 705
Db 601 GCAAGCAGCAGAGCCCAUGGAGGUGUUAUUGGCGUUAUUGGCAACCUUGGCAAGGAGUAG 660
Qy 706 AACCAUUGGACUUAUUGGCGUUAUUGGCGUUAUUGGCGUUAUUGGCGUUAUUGGCGUUA 765
Db 661 AACCAUUGGCGUUAUUGGCGUUAUUGGCGUUAUUGGCGUUAUUGGCGUUAUUGGCGUUA 720
Qy 766 GCAGGCGUUAUUGGCGUUAUUGGCGUUAUUGGCGUUAUUGGCGUUAUUGGCGUUAUUGG 819
Db 721 GCAGGCGUUAUUGGCGUUAUUGGCGUUAUUGGCGUUAUUGGCGUUAUUGGCGUUAUUGG 774

RESULT 3
US-10-177-390-31
; Sequence 31, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:

; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Influenza virus
US-10-177-390-31

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Query Match      81.2%; Score 764.6; DB 6; Length 1027;
Best Local Similarity 76.6%; Pred. No. 5.4e-177;
Matches 597; Conservative 173; Mismatches 9; Indels 0; Gaps 0;

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Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
16 ATATTGAAGATGAGTCTTCTAAACGAGGTGAAACGTAAGTCTCTATCATCCCGTC 75

Qy 106 AGGCCCCCUCAAAGCGGAGUAGCAGAGACGUAAGAGUUCUUGCAGGGAAGAACAC 165
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
76 AGGCCCCCTCAAAGCGGAGATCGCACAGAGACTTGAAGATGCTTTGCGAGGGAAGAACAC 135

Qy 166 CGAUCUUGAGGUCUUAUGGAUUGGCUAAGACAGACCAUUCUUGUACCUUGACUUA 225
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
136 CGATCTTGGAGTTCTCATGGAATGGCTTAAGACAGAACCAATCTCTGACCTCTGACTAA 195

Qy 226 GGGGAUUAUAGGUAUUGUUCACGUCACCGUGCCGAGGAGCGAGGACGCGGAG 285
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
196 GGGGATTTAGGATTTGTTCAAGCTCAGCTCAGCTGCCAGTGAAGAGACTGCGAGCGTAG 255

Qy 286 ACGCUUUGUCCAAAGUCCUUAUUGGAAACGGGGAUCCAAUUAACAUUGGACAAAGCAGU 345
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
256 ACGCTTTGTCAAATGCGCTTAATGGGAACGGGGATCCAAATAAATGGAACAAAGCAGT 315

Qy 346 UAAACUUAUAGGAAGCUCAGAGGAGAGUAACAUUCUUGGCGCCAAAGAAUUCUACU 405
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
316 TAAACTGTATAGGAAGCTCAAGAGGAGATTAACATTCATGGGCGCCAAAGAAATCTCACT 375

Qy 406 CAGUUAUUCUGGUGGCAUUGGCGUUGGUAUGGCAACUUGGAAACAGAUUGCGACUC 525
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
436 TGTGACCACTGAAGTGGCATTTGGCTGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy 526 CGAGCAUGGUCUUAUGGCAUUGGUGAUAACCAACCAACCAUUAUCAGACAUGAGAA 585
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
496 CCAGCATCGGTCTCATAGGCAAAATGGTGAACAAACCAACCACTAATCAGACATGAGAA 555

Qy 586 CAGAAUGUUAUAGCCACACUACAGCUAGGCUAGGAGCAAAUGGUGGAGUAGGAGUGA 645
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
556 CAGAAUGUUAUAGCCACACUACAGCUAGGCUAGGAGCAAAUGGUGGAGUAGGAGUGA 615

Qy 646 GCAAGCAGCAGAGGCGCAUUGGAGGUAAGGCAAAUGGUGGAGUAGGAGUAG 705
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
616 GCAAGCAGCAGAGGCGCAUUGGAGGUAAGGCAAAUGGUGGAGUAGGAGUAG 675

Qy 706 AACCAUUGGAGCUCUAUUCUAGCUCAGUUGGUGUAGAAUUAUUCUUGAAUUAU 765
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
676 AACCAUUGGAGCUCUAUUCUAGCUCAGUUGGUGUAGAAUUAUUCUUGAAUUAU 735

Qy 766 GCAGGCCUUAUCAGAAACGAUUGGCGGUGCAGUACGUAACGUAUUCUAGUACU 824
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
736 GCAGGCCUUAUCAGAAACGAUUGGCGGUGCAGUACGUAACGUAUUCUAGUACU 794
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US-10-855-875-5
; Sequence 5, Application US/10855875
; Publication No. US20050003349A1
; GENERAL INFORMATION:
; APPLICANT: Kawasaka, Yoshihiro
; TITLE OF INVENTION: High Titer Recombinant Influenza Viruses for Vaccines and Gene
; FILE REFERENCE: 800.038US1
; CURRENT APPLICATION NUMBER: US/10/855,875
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: US 60/473,798
; PRIOR FILING DATE: 2003-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Influenza virus
US-10-855-875-5

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Query Match      80.8%; Score 761.4; DB 8; Length 1027;
Best Local Similarity 76.5%; Pred. No. 3.3e-176;
Matches 596; Conservative 172; Mismatches 11; Indels 0; Gaps 0;

Qy 46 AGAUCUAAAGUAGUCUUAACCGAGGUGGAAACGUAACGUUCUCUUAUCCGCCGUC 105
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
16 ATATTGAAGATGAGTCTTCTAAACGAGGTGAAACGTAAGTCTCTATCATCCCGTC 75

Qy 106 AGGCCCCCUCAAAGCGGAGUAGCAGACAGACUUAAGAGUUCUUGCAGGGAAGAACAC 165
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
76 AGGCCCCCTCAAAGCGGAGATCGCACAGAGACTTGAAGATGCTTTGCGAGGGAAGAACAC 135

Qy 166 CGAUCUUGAGGUCUUAUGGAUUGGCUAAGACAGACCAUUCUUGGAGGAGUAGGAGUAG 225
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
136 CGATCTTGGAGTTCTCATGGAATGGCTTAAGACAGAACCAATCTCTGACCTCTGACTAA 195

Qy 226 GGGGAUUAUAGGUAUUGUUCACGUCACCGUGCCGAGGAGCGAGGACGCGGAG 285
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
196 GGGGATTTAGGATTTGTTTTCAGCTCAACGTCGCCAGTGAAGAGACTGCGAGCGTAG 255

Qy 286 ACGCUUUGUCCAAAGUCCUUAUUGGAAACGGGGAUCCAAUUAACAUUGGACAAAGCAGU 345
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
256 ACGCTTTGTCAAATGCGCTTAATGGGAACGGGGATCCAAATAAATGGAACAAAGCAGT 315

Qy 346 UAAACUUAUAGGAAGCUCAGAGGAGAGUAACAUUCUUGGCGCCAAAGAAUUCUACU 405
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
316 TAAACTGTATAGGAAGCTCAAGAGGAGATTAACATTCATGGGCGCCAAAGAAATCTCACT 375

Qy 406 CAGUUAUUCUGGUGGCAUUGGCGUUGGUAUGGCGCCUUAUUAACAGGAUUGGCGGC 465
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
376 CAGTTATTTCTGCTGGTGCACTTGGCAGTTGTATGGGCTCATATACAACAGGATGGGGC 435

Qy 466 UGUGACCAUUGAAGGUGCAUUGGCGUUGGUAUGGCAACUUGGAAACAGAUUGCGACUC 525
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
436 TGTGACCACTGAAGTGGCATTTGGCTGTATGTGCAACCTGTGAACAGATTGCTGACTC 495

Qy 526 CGAGCAUGGUCUUAUGGCAUUGGUGAUAACCAACCAACCAUUAUCAGACAUGAGAA 585
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
496 CCAGCATCGGTCTCATAGGCAAAATGGTGAACAAACCAACCACTAATCAGACATGAGAA 555

Qy 586 CAGAAUGUUAUAGCCACACUACAGCUAGGCUAGGAGCAAAUGGUGGAGUAGGAGUGA 645
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
496 CCAGCATCGGTCTCATAGGCAAAATGGTGAACAAACCAACCACTAATCAGACATGAGAA 555

Qy 646 GCAAGCAGCAGAGGCGCAUUGGAGGUAAGGCAAAUGGUGGAGUAGGAGUAG 705
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
556 CAGAAUGUUAUAGCCACACUACAGCUAGGCUAGGAGCAAAUGGUGGAGUAGGAGUGA 615

Qy 706 AACCAUUGGAGCUCUAUUCUAGCUCAGUUGGUGUAGAAUUAUUCUUGAAUUAU 765
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
616 AACCAUUGGAGCUCUAUUCUAGCUCAGUUGGUGUAGAAUUAUUCUUGAAUUAU 675

Qy 766 GCAGGCCUUAUCAGAAACGAUUGGCGGUGCAGUACGUAACGUAUUCUAGUACU 824
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
766 GCAGGCCUUAUCAGAAACGAUUGGCGGUGCAGUACGUAACGUAUUCUAGUACU 824
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; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
; US-10-065-133A-1

Query Match      68.7%; Score 647.4; DB 6; Length 1023;
Best Local Similarity 70.8%; Pred. No. 2.8e-148;
Matches 546; Conservative 148; Mismatches 77; Indels 0; Gaps 0;

Qy 46 AGAUCUAAAGUAGUUCUUAACCGAGGUCGAAACGUAUUCUUCUUAUCCGUC 105
Db 15 ATATTTAAAGATGAGTCTTCTGACCGAGGTGAAACGTAGCTTCTCTATCGTACC 74

Qy 106 AGGCCCCUCAAAGCCGAGUCCGACAGAGACUUGAAGUUCUUAUCCGAGGAGAACAC 165
Db 75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCGAGGAGAACAC 134

Qy 166 CGAUUUGAGGUUCUUAUGGAAUAGGCUAAAGACAAUCCUUGUCUACCCUCUGACUAA 225
Db 135 CGATCTTGAGGCACTCATGGAATGGCTTAAAGACAAGACCAATCTGTCTCTGACTAA 194

Qy 226 GGGGAUUUAGGAUUUGUUCACGUCUACCGUGCCGAGAGGAGGAGUUCGACGCUAG 285
Db 195 AGGGATTTTGGATTCGTATTCACGCTCACCGTCCGAGGAGGAGCTGCGAGCGTAG 254

Qy 286 AGCUUUGUCCAAAGUCCUUAUUGGGAACGGGGAUCCAAUAAACGAGGAGGAGUUCGAC 345
Db 255 AGCTTTTGTCCAAATGCGCTTAGTGGAAACGGAGATCCAAACACATGACAGAGCAGT 314

Qy 346 UAAACUGUUAAGGAGGCUAAGGAGGAGUAAUUAUCCAUUGGGGCCAAAGAAUUCUACU 405
Db 375 CAGCTATTCCACTGGTGCATAGCGCTTAAAGCCATGAGGAGGAGTGGCAGGTCGAGTGA 434

Qy 466 UGUGACCAUAGGAGGUUUGUUCACGUCUACCGUCCGAGGAGGAGGAGGAGGAGGAG 525
Db 435 TGTGACAAACCGAAGTGGCATTTGGCCCTGGTATGGCCACATGTGAACAGATCGTGATTC 494

Qy 526 CCAGAUUCGUGUUAUAGGAAUUGGUGAUAUUAUCCAUUGGGGCCAAAGAAUUCUACU 585
Db 495 CCAGATCGATCTCACAGGCGAGATGGTGAACAACAACCCATTAATCAGACATGAA 554

Qy 586 CAGAAUGUUUUAUCCGAGCAGUACAGCUAAGGCUUAUUGGAGGAGGAGGAGGAGGAG 645
Db 555 CAGAAUGGATTTAGCCAGTACCGGCTTAAGCCCATGGAGGAGATGGCAGGTCGAGTGA 614

Qy 646 GCAAGCAGCAGAGGCCCAUUGGAGGUGUUCUAGUGGCGUAGGCAAAUUGGUGCAUGAG 705
Db 614 GCAAGCAGCAGAGGCCCAUUGGAGGUGUUCUAGUGGCGUAGGCAAAUUGGUGCAUGAG 705

; RESULT 9
; US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; Education
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; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-CI-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (663)..(663)
; OTHER INFORMATION: At nucleotide 663, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
; US-10-434-811A-1
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Query Match      68.7%; Score 647.4; DB 7; Length 1023;
Best Local Similarity 70.8%; Pred. No. 2.8e-148;
Matches 546; Conservative 148; Mismatches 77; Indels 0; Gaps 0;

Qy 46 AGAUCUAAAGUAGUUCUUAACCGAGGUCGAAACGUAUUCUUCUUAUCCGUC 105
Db 15 ATATTTAAAGATGAGTCTTCTGACCGAGGTGAAACGTAGCTTCTCTATCGTACC 74

Qy 106 AGGCCCCUCAAAGCCGAGUCCGACAGAGACUUGAAGUUCUUAUCCGAGGAGAACAC 165
Db 75 AGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGCGAGGAGAACAC 134

Qy 166 CGAUUUGAGGUUCUUAUGGAAUUGGUGAUAUUAUCCAUUGGGGCCAAAGAAUUCUACU 225
Db 135 CGATCTTGAGGCACTCATGGAATGGCTTAAAGACAAGACCAATCTGTCTCTGACTAA 194

Qy 226 GGGGAUUUAGGAUUUGUUCACGUCUACCGUCCGAGGAGGAGGAGGAGGAGGAG 285
Db 195 AGGGATTTTGGATTCGTATTCACGCTCACCGTCCGAGGAGGAGCTGCGAGCGTAG 254

Qy 286 AGCUUUGUCCAAAGUCCUUAUUGGGAACGGGGAUCCAAUAAACGAGGAGGAGUUCGAC 345
Db 255 AGCTTTTGTCCAAATGCGCTTAGTGGAAACGGAGATCCAAACACATGACAGAGCAGT 314

Qy 346 UAAACUGUUAAGGAGGCUAAGGAGGAGUAAUUAUCCAUUGGGGCCAAAGAAUUCUACU 405
Db 315 AAAAAGTGTACAGGAAGCTTAAAGAGAGAAATAACATTCATCGGGGCCAAAGAGGTGGCACT 374

Qy 406 CAGUUAUUCUGUGGUCUACUUGCCAUUUGGCGUUAUUGGCGCUUAUUAACAGGAGGAGG 465
Db 375 CAGCTATTCCACTGGTGCATAGCGCTTAAAGCCATGAGGAGGAGTGGCAGGTCGAGTGA 434

Qy 466 UGUGACCAUAGGAGGUUUGUUCACGUCUACCGUCCGAGGAGGAGGAGGAGGAGGAG 525
Db 435 TGTGACAAACCGAAGTGGCATTTGGCCCTGGTATGGCCACATGTGAACAGATCGTGATTC 494

Qy 526 CCAGAUUCGUGUUAUAGGAAUUGGUGAUAUUAUCCAUUGGGGCCAAAGAAUUCUACU 585
Db 495 CCAGATCGATCTCACAGGCGAGATGGTGAACAACAACCCATTAATCAGACATGAA 554

Qy 586 CAGAAUGUUUUAUCCGAGCAGUACAGCUAAGGCUUAUUGGAGGAGGAGGAGGAGGAG 645
Db 555 CAGAAUGGATTTAGCCAGTACCGGCTTAAGCCCATGGAGGAGATGGCAGGTCGAGTGA 614

Qy 646 GCAAGCAGCAGAGGCCCAUUGGAGGUGUUCUAGUGGCGUAGGCAAAUUGGUGCAUGAG 705
Db 614 GCAAGCAGCAGAGGCCCAUUGGAGGUGUUCUAGUGGCGUAGGCAAAUUGGUGCAUGAG 705
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Db 75 AGGCCCCCTCAAGCCGAGATCGCGCAGAGACTTGAAGATGCTTTTGAGGGGAAGAACAC 134
Qy 166 CGAUUUGAGGUUCUUAUGGAUUGGCUAAAGACAAGACCAAUUCUGUCACCUUCUGACUAA 225
Db 135 CGATCTTGAGGCATCATGGAATGGCTAAGACAAGACCAATCTGTCACTCTGACTAA 194
Qy 226 GGGGAUUUAGGAUUUGUUGUUCACGUCUACCGUGCCAGUGAGCGAGACUGCGAGUAG 285
Db 195 AGGGAUUAAGGATTCGTATTACGCTCACCGTCCAGTCCAGTGGAGGAGCTGCAGCGTAG 254
Qy 286 AGCUUUGUCCAAAUUGCCUUAUUGGAAGCGGAGUCCAAUUAACAUUGGACAAAGCAGU 345
Db 255 AGCTTTTGTCCAAATGCCCTTAGTGAACCGAGATCCAAACCAACATGGCAGACAGT 314
Qy 346 UAAACUGUAUAGGAAGUCUAGAGGAGAGUAUACAUUCUAGUGGCGCCAAAGAAUUCACU 405
Db 315 AAAACTGTACAGGAAGCTTAAAGAGAAATACATTCATGGGCGCAAAAGAGGTGGCACT 374
Qy 406 CAGUUUUCUGCUGUGCACAUUGCCAGUUGUAUUGGGCCUCUAUAUACAAACAGGAUGGGGC 465
Db 375 CAGCTATTCCACTGGTCACTAGCCAGCTGCTGGGACTCATATACAAACAGAAATGGGAAC 434
Qy 466 UGUGACCAUUAAGUGGCAUUGCCUGGUUAUGGCAACUUGUAAACAGAUUGCUGACUC 525
Db 435 TGTGACAAACGAATGGGCAATTTGGCTGTGTATGCGCCACATGTGAACAGATCGCTGATTC 494
Qy 526 CCAGCAUCGUCUUAUAGGCAAAUUGGUGAGCAACCAACCAACCAUUAUUCAGACAUGAGAA 585
Db 495 CCAGCATGATCTCACAGGAGATGGTGACAAACCAACCAACCCATTATCAGACATGAAGA 554
Qy 586 CAGAAUGUUUAGCCAGCACUAACAGUAAAGGUUAUGAGCAAAUUGGUGAGUAGCAGUGA 645
Db 555 CAGAATGGTATTAGCCAGTACCAAGCTTAAGCCATGGAGCAGATGGCAGGTCGAGTGA 614
Qy 646 GCAGCAGCAGAGCCAGGAGGUUGUUGCAGGUAGGCAUAGGCAAAUUGGUGAGCAGUAG 705
Db 615 GCAGGCGCAGAGGCCATGGAGGTTGTAGTAGTAAAGCTAGGCGAGATGGTTCACAAATGAG 674
Qy 706 AACCAUUGGGACUACUACGUCUAGCAGUGCUGUGUCUAGAAAUUGAUUUCUUGAAAUUU 765
Db 675 AACCATTTGGGACCCACCTAGCTCCAGTGCCGGTTTGAAGATGATCTCTTGAATAATT 734
Qy 766 GCAGGCUUACAGAAACGAUUGGGGUGCAGUAGCAACGGUUCUAAUGUAAAC 816
Db 735 GCAGGCUUACAGAAACGAUUGGGGAGTGCAAAATGCGAGATTCAAGTGATC 785
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RESULT 12

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US-09-747-335-3
; Sequence 3, Application US/09747335
; Patent No. US20020095692A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, David
; APPLICANT: Skinner, Anita
; APPLICANT: Hay, Alan
; TITLE OF INVENTION: Conditional Mutants of Influenza Virus M2 Protein
; FILE REFERENCE: 18396/1500
; CURRENT APPLICATION NUMBER: US/09/747,335
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/GB99/02204
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: GB 98150040.2
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Influenza A virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(26)
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; OTHER INFORMATION: Exon
; NAME/KEY: misc feature
; LOCATION: (715)..(982)
; OTHER INFORMATION: Exon
US-09-747-335-3
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Query Match 68.6%; Score 645.8; DB 3; Length 1002;

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Best Local Similarity 69.3%; Pred. No. 6.9e-148; Indels 0; Gaps 0;
Matches 533; Conservative 159; Mismatches 77;
Qy 56 AUGAGUUCUUAACACCGAGGUCGAAAGCUUUCUUAUACUCCGUGCAGGCCCCUC 115
Db 1 ATGAGTCTTCTAACCGAGGTTGAAACGAGTCTCTCTATCATCCATCAGGCCCTC 60
Qy 116 AAAGCCGAGAUCCGACAGAGACUUGAAGUUCUUGCAGGGAAGAACCGCAUCUUG 175
Db 61 AAAGCCGAGATCGCGAGAGACTTGAAGATGTCTTTCAGGGGAAAAACACAGACCT 120
Qy 176 GUUCUCAUGGAUUGGCUAAGACAAAGACCAUUCUCCUACUAGCUAAAGGGGAUUUA 235
Db 121 GTTCTCATGAATGGCTTAAAGACAAGACCAATCTGTCACTCTGACTAAAGGATTTG 180
Qy 236 GGAUUUGUUCACGUCACCGUGCCAGUGAGCGAGGACUGCAGCGUAGACGCUUUG 295
Db 181 GGGTTTGTGTTACGCTCACCGTCCAGTGAGCAAGGACTGCAGCGTAGACGCTTGT 240
Qy 296 CAAAUAUGCCCUUUAUGGGAACCGGGGAUCCAAUAUACUUGGACAAAGCAGUUAA 355
Db 241 CAAAATGCCCTAAATGGGAATGGGATCCAAATAACATGATGAAGCGCTCAAACTAT 300
Qy 356 AGGAGCUCUAAGAGGGAGUAACAUIUCUUGGGGCCAAAGAAUUCACUACUUAUUC 415
Db 301 AGGAAGTTGAAAGGGAGATAACATTTCTATGGAGCTTAAGNAAGTGGCACTCAGT 360
Qy 416 GCUUGGCAUCUUGCCAGUUGUAUUGGCGCUCAUAUACAACAGAGUUGGGGUGUAG 475
Db 361 ACTGGAGCACTTGCAGTTGTATGGGCTCATATACAACAGAACTGGGAACCTGTG 420
Qy 476 GAAGUGCAUUUGCCUUGUUAUGGCAACCUUGUAAACAGAUUGUGUACUCCAGCA 535
Db 421 GAGTGCATTTGGCCTTAGTGTGTGCACCTTGTGAGCAGATTGCTGATTCACAGCAT 480
Qy 536 UCUUAUAGGCAGAUUGGUCACAAACCAACCCUAAUACAGAUAGAGAAAGAAUGGU 595
Db 481 TCTCAGACAGATGTTGGCTACACCAATCTCACTATCAGGCATGAGAACAGAAATG 540
Qy 596 UUAGCCAGCACUACAGCUAAGGCUUAGGAGCAAAUUGGCUAGUGAGGAGGAGAGCA 655
Db 541 ATGCCCAGCACTACAGCTAAGGCTATGGAGCAAAATGGCTCAATTGAACAGGCAG 600
Qy 656 GAGGCCAUGAGGUUGUAGUAGGCGCUAGGCAAAUUGGUGAGCGAUGAGAACCAUUG 715
Db 601 GAGGCCATGAGGTTGTAGCCAGGCTAGGAGATGTTGAGGCAATGAGGACAAATGG 660
Qy 716 ACUCUACUAGCUCUUGGUGUUGGCUUAGAAAUUGAUUUCUUGAAAAUUGCAGGCC 775
Db 661 ACTCATCTAGTCTCAGTGTGGTCTGAAGATGATCTTCTTGAATAATTTGAGGCT 720
Qy 776 CAGAAACGAAUUGGGGUGCAGAGCAACGGGUCAAGUUAAGUAAACUAGUGACU 824
Db 721 CAGAAACGGATGGGAGTGCAGATGCAACGATTCAGGTGACCTCTCTCAT 769
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RESULT 13

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US-10-435-723A-3
; Sequence 3, Application US/10435723A
; Publication No. US20040055024A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, David B
; APPLICANT: Skinner, Anita
; APPLICANT: Hay, Alan J
; TITLE OF INVENTION: Conditional Mutants of Influenza Virus M2 Protein
; FILE REFERENCE: 18396/1503
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Db      495  CCAGCATCGATCTCACAGGCAGATGGTGACAAATACCAACCCATTAAATCAGACATGAAAA 554
Qy      586  CAGAAUGUUUAGCCAGCACUACAGCUAAGGCUAUGGACAAAUUGGCUUGAGUUGGAGUGA 645
Db      555  CAGAAUGGATATTAGCCAGTACCAAGGCTAAAGCCATGGAGCAGATGGCAGGTCGAGTGA 614
Qy      646  GCAAGCAGCAGAGCCAGGAGGUGUUGUAGUCAGGCUAGGCAAAUUGGCUAGGAGGAG 705
Db      615  GCAGGCAGCAGAGCCAGGAGGTTGCTAGTAAGGCTAGGACGATGGTACAGGCAATGAG 674
Qy      706  AACCAUUGGACUACUAGCUCAGCUCAGGUCUGGUCUGAAGGAGGAGGAGGAGGAGGAG 765
Db      675  AACCAUUGGAGCCACCCCTAGTCCAGTGCGGTTGAAAGATGATCTCTTGAATAATTT 734
Qy      766  GCAGGCUUACAGAAACGAAUUGGAGGUGCAGAUCAACCGGUCUUAAGUGAAG 816
Db      735  GCAGGCCTACAGAAACCGGATGGAGTGCAAAATGCAGCGATTCAGATGATC 785

RESULT 15
US-10-434-811A-4
; Sequence 4, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; Education
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-CL-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
US-10-434-811A-4

Query Match      68.4%; Score 644.6; DB 7; Length 1023;
Best Local Similarity 70.7%; Pred. No. 1.4e-147;
Matches 545; Conservative 147; Mismatches 79; Indels 0; Gaps 0;

Qy      46  AGAUUAAAGAUAGAGUCUUAUACGAGGUGGAAACGUACUUCUCUUAUUAUCCCGUC 105
Db      15  ATATTAAAGATGATGCTCTGACCGAGGTGAAACGTACGTTCTCTATCTTACCATC 74
Qy      106  AGGCCCCUCUAAAGCCGAGUUGCAGAGACUUGAAGUUGUUGCAGGAGAAACAC 165
Db      75  AGGCCCCCTCAAGCGAGATCGCGCAGAGACTTGAAGATGCTTTGCGAGGAGAAACAC 134
Qy      166  CGAUUUGAGGUUUCUAGGAAUUGGCUAAGACAAAGACCAUCCUUGUACCUUGACUAA 225
Db      135  CGATCTTGAGGCACTCATGGAATGGCTAAAGACAAAGCAATCTGTCACTCTGACTAA 194
Qy      226  GGGGAUUUAGGAUUUGUUCACGUCACGUGCCAGUGAGCGGAGGAGGAGGAGCGUAG 285
Db      195  AGGATTTTAGATTCGTATTTCACGCTCACCGTCCCGGAGTGAAGGAGACTGCGAGCTAG 254
Qy      286  ACGUUGUCCAAAAGUCCCUUAAUUGGAAACGGGGAUCCAAAUAAUAGGACAAAGCAGU 345
Db      255  ACGCTTTGTCAAAATGCCCCTTAGTGGAAACGGAGATCCAAACAAACATGGACAGGAGT 314
Qy      346  UAAACUGUUAAGGAGGCUAAGAGGAGGAGAAUACAUUCCUUGGGGCGCAAGAAUUCUCACU 405

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Db      315  AAAACTGTACAGGAAGCTTAAAGAGAGAAATAACATTCATGGGCGCAAAAGAGGTGGCACT 374
Qy      406  CAGUUAUUCUGUGGUCACUUGCCAGUUGUUAUUGGGCCUUAUUAACAACAGGAUGGGGGC 465
Db      375  CAGCTATTCACCTGGTGCACTAGCCAGCTGCATGGGACTCATATACAACAGAAATGGGAAC 434
Qy      466  UGUGACCAUUGAAGUGGCAUUGGCGGCUUGUUGCAACCUUGUGAACAGAUUCGUCACUC 525
Db      435  TGTGACAAACGAAAGTGGCATTTGGCTGTGTATCGGCCACATGTGAACAGATCGCTGATTC 494
Qy      526  CCAGCAUCGGUCUCUAGGCAAAUUGGACAAACCAACCAACCCACUAAUACAGACAUAGAA 585
Db      495  CCAGCATCGATCTCACAGGCAGATGGTGACAAATAACCAACCCATTAAATCAGACATGAAA 554
Qy      586  CAGAAUGUUUUGAGCAGCAGCUACAGCUAAGGCUAUGGAGCAAAUUGGCUUGGAGUGA 645
Db      555  CAGAAUGGATATTAGCCAGTACCAACGGCTAAAGCCATGGAGCAGATGGCAGGTCGAGTGA 614
Qy      646  GCAAGCAGCAGAGCCCAUGGAGGUGUUGCUAGUCAGGCUAGGCAAAUUGGCUAGGAGGAG 705
Db      615  GCAGGCAGCAGAGGCGCCATGGAGGTTGCTAGTAAGGCTTAGGCAGATGGTACAGGCAATGAG 674
Qy      706  AACCAUUGGAGCUCUACUAGCUCUAGCUCGAGGUCUGUAAAAUUAUUAUUAUUAUUAU 765
Db      675  AACCAUUGGAGCCACCCCTAGTCCAGTGCGGTTTGAAGATGATCTCTTGAATAATTT 734
Qy      766  GCAGGCUUACAGAAACGAAUUGGAGGUGCAGAUCAACCGGUCUUAAGUGAAG 816
Db      735  GCAGGCCTACAGAAACCGGATGGAGTGCAAAATGCAGCGATTCAGATGATC 785

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Job time : 927.936 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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(without alignments)
5130.555 Million cell updates/sec

Title: US-10-729-830-5

Perfect score: 942

Sequence: 1 gcuugucuuuugcagaag.....aaaaaaaaaaaaaaaaaaaa 942

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:*

- 1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB_seq.*
- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB_seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB_seq.*
- 4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB_seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB_seq.*
- 6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB_seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB_seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB_seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB_seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB_seq2.*
- 11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB_seq3.*
- 12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB_seq4.*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB_seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	758.2	80.5	1027	12	US-11-131-479-3		Sequence 3, Appli
2	749.6	79.6	1305	12	US-11-131-479-45		Sequence 45, Appl
3	700.2	74.3	987	12	US-11-155-478A-131		Sequence 131, App
4	689.4	73.2	1027	12	US-11-155-478A-130		Sequence 130, App
5	681.6	72.4	4822	12	US-11-131-479-95		Sequence 95, Appl
6	681.6	72.4	7798	12	US-11-131-479-97		Sequence 97, Appl
7	681.6	72.4	7798	12	US-11-131-479-98		Sequence 98, Appl
8	681	72.3	982	12	US-11-131-479-60		Sequence 60, Appl
9	681	72.3	5161	12	US-11-131-479-101		Sequence 101, App
10	681	72.3	5398	12	US-11-131-479-91		Sequence 91, Appl
11	681	72.3	7798	12	US-11-131-479-99		Sequence 99, Appl
12	681	72.3	7798	12	US-11-131-479-100		Sequence 100, App
13	681	72.3	8442	12	US-11-131-479-106		Sequence 106, App
14	681	72.3	8442	12	US-11-131-479-107		Sequence 107, App
15	681	72.3	8450	12	US-11-131-479-104		Sequence 104, App
16	681	72.3	8450	12	US-11-131-479-105		Sequence 105, App
17	526.6	55.9	629	9	US-11-137-807-18		Sequence 18, Appl
18	502	53.2	982	12	US-11-131-479-61		Sequence 61, Appl
19	501.4	53.2	759	12	US-11-131-479-79		Sequence 79, Appl
20	474.4	50.4	756	12	US-11-131-479-27		Sequence 27, Appl

21	471.2	50.0	756	12	US-11-131-479-28		Sequence 28, Appl
22	464	49.3	1050	12	US-11-131-479-59		Sequence 59, Appl
23	459.8	48.8	759	12	US-11-131-479-69		Sequence 69, Appl
24	447.8	47.5	756	12	US-11-131-479-26		Sequence 26, Appl
25	477.4	8.2	1180	12	US-11-116-746-2		Sequence 2, Appli
26	77.4	8.2	1180	12	US-11-116-746-4		Sequence 4, Appli
27	75.8	8.0	588	12	US-11-136-527-1488		Sequence 1488, Ap
28	75.8	8.0	588	12	US-11-136-527-5584		Sequence 5584, Ap
29	75.2	8.0	1677	7	US-10-515-547-3		Sequence 3, Appli
30	75.2	8.0	4339	8	US-10-909-125-801		Sequence 801, App
31	74.8	7.9	2475	9	US-11-197-133A-17		Sequence 17, Appl
32	74.8	7.9	5152	8	US-10-240-708-47		Sequence 47, Appl
33	74.6	7.9	1395	8	US-10-955-054A-111		Sequence 111, App
34	74.6	7.9	2217	8	US-10-947-249-197		Sequence 197, App
35	74.6	7.9	3819	7	US-10-973-115B-405		Sequence 405, App
36	74.6	7.9	3819	8	US-10-131-826A-405		Sequence 405, App
37	74.4	7.9	600	12	US-11-136-527-6371		Sequence 6371, Ap
38	74.4	7.9	2020	12	US-11-090-617-697		Sequence 697, App
39	74.4	7.9	3015	12	US-11-183-136-39		Sequence 39, Appl
40	74.4	7.9	4409	12	US-11-136-527-2275		Sequence 2275, Ap
41	74.2	7.9	1905	8	US-10-947-249-132		Sequence 132, App
42	74	7.9	1690	12	US-11-090-439-43		Sequence 43, Appl
43	73.8	7.8	588	8	US-10-689-742-41		Sequence 41, Appl
44	73.6	7.8	762	9	US-11-096-568A-12243		Sequence 12243, A
45	73.6	7.8	2845	7	US-10-973-115B-207		Sequence 207, App

ALIGNMENTS

RESULT 1
US-11-131-479-3
; Sequence 3, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Influenza A virus
US-11-131-479-3

Query Match	80.5%	Score 758.2;	DB 12;	Length 1027;
Best Local Similarity	76.3%	Pred. No. 2.4e-84;		
Matches	594;	Conservative 172;	Mismatches 13;	Indels 0; Gaps 0;
Qy	46	AGAUCAAAGAUGAGUCUUAACCGGAGGUGCGAAACGUAACGUCUUAUCCGUC	105	
Db	16	ATATTGAAGATGAGTCTTCTACCGAGGTCGAAACGTACGTCTCTCTATCATCCGTC	75	
Qy	106	AGGCCCCCAAGCCGAGGAGCGACAGACUUAAGAGUUCUUAUCCGAGGAGAACAC	165	
Db	76	AGGCCCCCTCAAGCCGAGATCGCACAGAGATGTCTTTCGAGGAGAACAC	135	
Qy	166	CGAUUUGAGUUCUUAAGAGGCUUAAGACAAAGACACUUAUCCGAGGAGAACAC	225	
Db	136	TGATCTTGAAGTCTCTAAGTAAGGCTTAAGACAAAGACAACTCTGTACCTCTGACTTA	195	
Qy	226	GGGGAUUUAGGAUUUGUUCACGUCACCGUGCCAGAGGAGGAGGAGGAGGAGGAG	285	

196	GGGGATTTTAGGATTTGTGTTCA	CGCTCACGTCGCCAGTGAGCGAGAGCTGCACGGTAG	255
286	ACGCUUUGUCCAAAUAUGCCUUAAUUGGNAACGGGGAUCCAAUAA	CAUUGGCAAAAGCAGU	345
256	ACGCTTTGTCCAAAATGCCCTTAATGGGNAACGGGGATCCAAA	TACATGGACAAAGCAGT	315
346	UAAACUGUAUAGGAAGCUCAAAGGAGGAUAACAUAUCCAUUGGGGCCAAAGAAUUCUACA	U	405
316	TAAACTGTATAGGAAGCTCAAGAGGAGAGATAACAATTCCATGGGGCCAAAGAAATCTCACT		375
406	CAGUUAUUUCUGCGUGGACAUUGCCAUUGUAUUGGGCCUCAUAUAACAACAGGAUUGGGGGC		465
376	CAGTTATTCGTCTGCTGTCATTTGCCAGTTGTATGGGCGCTCATATACAACAGGATGGGGGC		435
466	UGUGACACACUGAAGUGGCAUUUGGCCUGGUAUGUCAAACCCUGUGAACAAGAUUGCUGACAUC		525
436	TGTGACCACTGAACTGGGCAATTTGGCGCTGGTATGTGCAACCTGTGAAACAGATGCTGACTC		495
526	CCAGCAUGGUCUCAUAGGCAAAUUGGUGACAAACAACCAACCAUAUUCAGACAUGAGAA		585
496	CCAGCATCGGTCTCATAGGCAAAATGGTGACAACAACCAACTCCACTTAATCAGACATGAGAA		555
586	CAGAAUGUUUAGCCAGCACUAACAGCUAAGCCUAUGGAGCAAAUUGGCUUGAUCAGUGA		645
556	CAGAATGGTTTTAGCGACACACTACAGCTAAGGCTATGGAGCAAAATGGCTGGATCCAGTGA		615
646	GCAAGCAGCAGAGGCCAUGGAGGUUGCUAGUCAGCUAGGCAAGGCAAAUUGGCUAGCAGCAUGAG		705
616	GCAAGCAGCAGAGGCCATGGAGGTTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAG		675
706	AACCAUUGGGGACUCAUCCUAGCUCACUGGCUUGGUGGAAAAAUAUGAUUCUUUGUAAAAUUU		765
676	AACCATGGGGACTCATCTGCTCCAGTGCTGCTGGAATAATGATCTCTTTGAAAAATTT		735
766	GCAGGCCUUAUCAGAAAACGAUUGGGGGGUCAGAUACAACGGUUUCAAUGUAAACUAGUGACU		824
736	GCAGGCTTATCAGAAAACGAATGGGGGTGCAGATGCAACGGTTTCAAGTGAATCTCTCGCT		794

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RESULT 2
US-11-131-479-45
; Sequence 45, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 1305
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Influenza A Virus M1 Fused to Synthetic HBcAg
US-11-131-479-45

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116	Qy	AAAGCCGAGAUCCGACAGACUUGAAGAUUCUUUGCAGGAGAGACACGACUUCUGAG	176
61	Db	AAAGCCGAGATCGCACAGAGACTTGAAGATGCTCTTTTCAGGGAAGAACTGATCTTTGAG	120
176	Qy	GUUCUCAUGAAUUGGCUAAAGACAAGCAACAAUCCUGUCACCUCUCUGACUAAAGGGGAUUUUA	235
121	Db	GTTCCTCATGGNATGGCTTAAGACAAGACCAATCCTGTCACTCTGACTTAAGGGGATTTTA	180
236	Qy	GGAUUGUGUUCAGCGUACAACGUGGCCAGUGAGCGAGGACUGCAGCGUAGAGCGCUUUGUC	295
181	Db	GGATTTGTGTTCAAGCTCACCGTCCCGAGTGAGCGAGGACTGCAAGCGTAGACGCTTTGTTC	240
296	Qy	CAAAUUGCCCUAAUUGGGAACGGGGUACCAAAUAAACUAGGACAAAGCAGUUUAAAACUGUAU	355
241	Db	CAAAATGCCCTTAATGGNAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTAT	300
356	Qy	AGGAAGCUCUAGAGGGAGUAUAACUUCUUGGGGCCAAAGAAUUCUCACUCAGUUUAUUCU	415
301	Db	AGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAGTTATTCT	360
416	Qy	GCUGGACACUUGCCAGUUGUAGGGCCUCUAUAUACAACAGAUUGGGGUGUGACCAACU	475
361	Db	GCTGGTGCACTTGCAGTTGATGGGCTCATATACAACGATGGGGGCTGTGACCACT	420
476	Qy	GAAGUGCAUUUGGCCUGGUAGUGGCAACUCUGUAGAACAGAUUGUCACUCCAGCAUCGG	535
421	Db	GAAGTGGAATTTGGCCTGGTATGTGTAACCTGTGAAACAGATTGCTGACTCCAGCATCGG	480
536	Qy	UCUCAUAGGCNAUUGGUGACAAACCAACCAACCAUCUAUCAGACAGAAACAGAUUGGU	595
481	Db	TCTCATATGGCAAAATGGTGACAAACCAATCCACTAATCAGACATGAGAACAGAATGGTT	540
596	Qy	UUAAGCCAGCACUACAGCUUAGGCUUAGGAGCAAAUUGGUGGUAUCGAGUAGCAACGACGA	655
541	Db	TTAGCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGGATCGAGTGAGCAAGCAGCA	600
656	Qy	GAGGCCAUGAGGUUGUAGUCAGGCUAGGGCAAAUUGGUGCAAGCGAUGAGAACCAUUGGG	715
601	Db	GAGGCCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGTCAAGCGGATGAGAACCAATGGG	660
716	Qy	ACUCAUCUAGCUCAGUGGUGGUCUGAAAAUAGAUUCUUUUGAAAAUUUGCAGGCCUUAU	775
661	Db	ACTCATCTAGCTCCAGTGCTGGTCTGNAAAATGATCTTCTTGAAAAATTTGCGGCCCTAT	720
776	Qy	CAGAAAACGAUUGGGGUGCAGAUACAACGGUUCUACAG	811
721	Db	CAGAAAACGAATGGGGTGCAGATGCAACGGTTTCAAG	756

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RESULT 3
US-11-155-478A-131
; Sequence 131, Application US/11155478A
; Publication No. US20060014140A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE LAVAL
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 987
; TYPE: DNA

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; ORGANISM: human Influenza A virus
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)...(987)
; OTHER INFORMATION: human Influenza A virus
; OTHER INFORMATION: strain A/Charlottesville/31/95 (H1N1)
; OTHER INFORMATION: accession number af398876
US-11-155-478A-131

Query Match          74.3%; Score 700.2; DB 12; Length 987;
Best Local Similarity 73.7%; Pred. No. 2.7e-77;
Matches 561; Conservative 162; Mismatches 38; Indels 0; Gaps 0;

Qy 56 AUGAGUCUUAACCGAGGUGGAAACGUAUCGUUUCUUAUCCCGUAGCCCGCCCCCUC 115
Db 1 ATGAGTCTCTAACCGAGGTCGAAACGTACGTTCTCTATCGTCCGTCAGGCCCCCTC 60

Qy 116 AAAGCGAGUCCGACAGAGACUUGAAGUUCUUGUUGUUGUUGUUGUUGUUGUUG 175
Db 61 AAAGCGAGATCGCACAGAGACTTGAAGATGTTCTTTGCTGGAAGAACACCCGATCTTGAG 120

Qy 176 GUUCUCUAGGAUGGCUAAAGACAGACCAACUCCUGUCCACUCUGACUAAGGGGAUUUA 235
Db 121 GCTCTCATGGAGTGCTAAAGACAGACCGATCTGTCTCACCTCTGACTAAGGGGATTTTA 180

Qy 236 GGAUUUGUUCACGUCACCGUGCCGAGUGAGCGAGGACUGCGAGCGUAGACGCUUUGUC 295
Db 181 GGATTTGTTTCAGCTCACCCTGTCGCCAGTGAGCGAGGACTGCGAGCGTTTGTCT 240

Qy 296 CAAAAGUCCUUUAUUGGGAACGGGGAUCCCAAUAACAUGGACAAAGCAGUUUAACUGU 355
Db 241 CAAAATGCCCTTAATGGGAATGGGGATCCAAATAACATGAGCAGAGCAGTTAAACTGTAT 300

Qy 356 AGGAAGCUCAGAGGAGUAACAUCUCCNUGGGGCCAAAGAAUUCUACUCAGUUUAUCU 415
Db 301 AGAAAGCTTAAGAGGGAGATAACATTCATGGGGCCCAAGAAATAGCACTCAGTTATTCT 360

Qy 416 GCUGUGCACAUCUGGCGUUAUGGGCCUCAUAUACAACAGAGUUGGGGCGUGAGCCACU 475
Db 361 GCTGGTGCACTTGGCAGTTGTATGGGCTCATATACACAGATGGGGGCTGTGACCAACC 420

Qy 476 GAAGUGGCAUUGGCCUGGUAUGUAGCAACUGUGAACAGAUUGUGUACUCCAGCAUUGG 535
Db 421 GAATCAGCATTTGGCCTGATATGCGCAACCTGTGAACAGATTGCTGACTCCAGCATAAG 480

Qy 536 UCUCUAAGGCCAAUUGUGUAGACAAACCAACCAUUAUCAGACACAUGAGAACAGAAUGGU 595
Db 481 TCTCATAGGCAAAATGGTAACAAACCAACCAATCCATTATTAAGACATGAGAACAGAAATGTT 540

Qy 596 UUAAGCCAGCACUACAGGCUAUGGCUAUGGCAAAUUGGCUUGUAGGAGCAGAGCAGCA 655
Db 541 CTGGCCAGCACTACAGCTAAAGCTATGAGGCAATGGCTGGATCGATGTAACAGAGCT 600

Qy 656 GAGGCCAUGGAGGUUGUAGUAGGCUAGGCAAAUUGGCUAGGAGUAGAACCAUUGGG 715
Db 601 GAGGCCATGGAGGTTGCTAGTCAGGCCAGCAAAATGGTGCAGGCAATGAGAGCCATTGGG 660

Qy 716 ACUCAUCCUAGCUCUAGGUGUUGUAGAAAUUAUUAUUAUUAUUAUUAUUAUUAU 775
Db 661 ACTCATCTAGCTCTAGCACTGGTCTGAAAATAATGATCTCTTTGAAAATTTTGAGCGCCCTAT 720

Qy 776 CAGAAACGAUUGGGGUGGACAGACAAACCGUUAAGUAGAC 816
Db 721 CAGAAACGAATGGGGTGCAGATGCAACGATTCAAGTGATC 761
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RESULT 4
US-11-155-478A-130
; Sequence 130, Application US/11155478A
; Publication No. US20060014140A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE LAVAL

```
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING  
; TITLE OF INVENTION: RESPIRATORY VIRUSES  
; FILE REFERENCE: 6013-148US  
; CURRENT APPLICATION NUMBER: US/11/155.478A  
; CURRENT FILING DATE: 2005-06-20  
; PRIOR APPLICATION NUMBER: CA 2,411,264  
; PRIOR FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: CA 2,418,004  
; PRIOR FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994  
; PRIOR FILING DATE: 2003-12-19  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 130  
; LENGTH: 1027  
; TYPE: DNA  
; ORGANISM: human Influenza A virus  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1)...(1027)  
; OTHER INFORMATION: human Influenza A virus  
; OTHER INFORMATION: strain A/Hong Kong/1180/99 (H3N2)  
; OTHER INFORMATION: accession number af386771  
US-11-155-478A-130
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Query Match          73.2%; Score 689.4; DB 12; Length 1027;
Best Local Similarity 72.1%; Pred. No. 5.5e-76;
Matches 556; Conservative 164; Mismatches 51; Indels 0; Gaps 0;

Qy 46 AGAUCUUAAGAUGAGUCUUAACCGAGGUGGAAACGUAUGUUCUUAUCCCGUC 105
Db 16 ATATTGAAAGATGAGCCTTACCCGAGGTCGAAACGTATGTTCTCTATCGTTCCATC 75

Qy 106 AGGCCCCCUCAAAGCCGAGUCCGACAGAGACUUGAAGUUCUUAUGCAGGAAGACAC 165
Db 76 AGGCCCCCTCAAAGCCGAAATCGCGAGAGACTTGAAGATGTTCTTCTGGGAAACAC 135

Qy 166 CGAUUUGAGGUUCUUAUGGAUUGGCUAAGACCAAGACCAUCCUGUCUCCUAGACUA 225
Db 136 AGATCTTGAGGCTCTCATGGANTGGCTTAAGACNAGACCAATCCTGTCCCTCTGACTAA 195

Qy 226 GGGGAUUUAAGGAUUUGUUGUUAACGUCUACCGUGCCCGAGUGAGGAGUAGCGUAG 285
Db 196 GGGGATTTTAGGGTTTGTGTTCCGCTCACCGTCCCGCAGTGAGCGAGACTGCGAGCGTAG 255

Qy 286 ACGUUUUGUCCAAAUUGCCCUUAUUGGGAACGGGGAUCCCAAAUUAACAGACAAAGCAGU 345
Db 256 ACGCTTTGTCCAAATGSCCTCAATGGGAATGGGGATGCCAANTAAACATGGACAAAGCAGT 315

Qy 346 UAAACUUAUAGGAAGCUCAAAGGGAGUAACAUAUCCAUUGGGGCCAAAGAAUUCUACU 405
Db 316 TAAACTGTATGAANAACTTAAGAGGGAGATTAACATTCATGGGGCCCAAGANATAGCCT 375

Qy 406 CAGUUAUUCUGUGGUGCACUUGCCUAGUUAUGGGCCUCAUAUAACAAGGAGUUGGGGC 465
Db 376 CAGTTATTCTGCTGGTGCACCTTGCCAGTTGCATGGGCTCATATACAAATAGGATGGGGC 435

Qy 466 UGUACCAUAGAGUGSCAUUUGCCUGUUAUGGCAACCCUGUAGACAGAUUGCUGACUC 525
Db 436 TGTAAACCACTGAAGTGGCATTTTGGCCCTGTTATGTGCAACATGTGAAACAGATTTGCTGACTC 495

Qy 526 CCAGACUUGGCUUAUAGGCAAAUUGGUAACAACCAACCCACUUAUAGACAGAAUGA 585
Db 496 CCAGACAGGTTCTCATAGGCAATTTGGTGGCAACACCAATCCATTATTAAGACATAGAGA 555

Qy 586 CAGAAUGUUUAAGCCAGCAUAACAGCUAAGGCUUAUGGAGCAAAUGGUGGAGUAGUGA 645
Db 556 CAGAAUGTTTTGGCCAGCACTACAGCTAAGGCTATGGAGCAAAATGCTGATCAAGTGA 615

Qy 646 GCAGACGAGAGCCCAUGGAGGUUGUUAUCUAGGCUUAGGCAAAUGGUGGAGGCAUGAG 705
Db 616 GCAGGACGAGGAGCCATGGAGATTGTTAGTCAGGCCAGGCAAAATGTTGCGAGCAATGAG 675
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Qy 706 AACCAUUGGACUACUACUAGCUCAGCUGGUGGUGCAAAAUCAUUCUUGAAAAUUU 765
Db 676 AGCGTTGGGACTATCTAGCTCCAGTACTGGTCTAAGAGATGATCTTCTTGAATAATT 735
Qy 766 GCAGGCCUUAUCAGAAAAAGAAUUGGGGUGGAGAUCAACCGGUUUAAGUGAAC 816
Db 736 GCAGACCTATCAGAAACGGATGGGGGTGCAGATCAACGATTCAAGTGACC 786

RESULT 5
US-11-131-479-95
; Sequence 95, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 95
; LENGTH: 4822
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4764, Ligation of VR4756 RV-Sali into VR10682 RV
US-11-131-479-95

Query Match 72.4%; Score 681.6; DB 12; Length 4822;
Best Local Similarity 70.7%; Pred. No. 3.7e-75;
Matches 554; Conservative 166; Mismatches 64; Indels 0; Gaps 0;

Qy 33 GCUCACUUCUGGCAGACUUAAGAUAGUUCUUAACCGAGUGCGAAACGUAACGUUCUCU 92
Db 791 GATCAGATATCGAATTGCCACCACTAGAGCTTCTAACCAGGTGGAACGATGTTCTCT 850
Qy 93 CUUAUACCCGUCAGGCCCCUCUAAAGCCGAGAGUCGCAAGAGUAGUAGUUCUUG 152
Db 851 CTATCGTTCCATCAGCGCCCCCTCAAAGCCGAAATCGCGCAGAGACTTGAAGATCTCTT 910
Qy 153 CAGGGAAGAACACCGAUUCUAGGUCUUAUGGAUUGGCUAAAGACAGACCAUUCUCU 212
Db 911 CTGGGAAAAACACAGATCTTGAGGCTCTCATGGAATGGCTAAAGACAGACCAATCTCT 970
Qy 213 CACUCUCUGAACGAGGAAUUAAGAUUUGUUCUACGUCACCGUGCCAGUGCGAG 272
Db 971 CACCTCTGACTAAGGGGATTTGGGGTTGTGTTCACGCTCACCGTCCCGAGTGGCGAG 1030
Qy 273 GACUGCAGCGUAGCGUUCUUAUUGCAAAUUGCCUUAUGGAAACGGGUAUCAAUAACA 332
Db 1031 GACTGCGAGGTAGACGCTTGTCCAAATGCCCTCAATGGGAATGGGATCCAAATAACA 1090
Qy 333 UGGAACAAGCAGUUAACUGUAUAGAGCUUACAGGAGGAGUAUACAUCUUGGGGCCA 392
Db 1091 TGGCAGAGCAGTAAACTATATAGAAACTTAAAGAGGGAGATTACATTTCCATGGGCCA 1150
Qy 393 AAGAAAUUCUACUCAGUUAUUCUGUGGUGCAGUUGCCAGUUAUGGCGCCUUAUACA 452
Db 1151 AAGAAATAGCACTCAGTTATTTCTGCTGTGACCTTGGCAGTTGATGGGCTCATATACA 1210
Qy 453 ACAGAUUGGGGCGUGACACAGUAGGCUUAUUGGCGGUGUAGUAGUACCGUGAGAC 512
Db 1211 ACAGAAATGGGGCTGTAAACCACTGAAGTGGCTTTGGGCTTGTGTATGTGCAACATGTGAAC 1270
Qy 513 AGAUUGCUGACUCCAGCAUCGUGUCUUAUGGCAAAUUGGUAACAACCAACCCACUA 572
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Db 1271 AGATTCTGACTCCAGCACAGTCTCATAGGCAATGTGGCAACACCAATCCATTAA 1330
Qy 573 UCACAGAUGAGAAACAGAAUUGUUUAAGCCAGCAGCUACAGCUAAAGGCUUAGGACAAUUG 632
Db 1331 TAAGGCATGAGAACAGAAATGTTTGGCCAGCACTACAGCTAAGGCTATGAGCAATGG 1390
Qy 633 CUGGAUCGAGUGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 692
Db 1391 CTGGATCAAGTGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1450
Qy 693 UGCAAGCGAUGAGAAACCAUUGGAGCUCUACUAGCUCUAGCUCUAGCUCUAGCUCUAGCUC 752
Db 1451 TGCAGGCAATGAGAGCAATTTGGGACTCATCTAGCTCCAGTGTGTCTTAAAGATGATC 1510
Qy 753 UUCUAGAAAAUUGCAGGCGCUUAUCAGAAAAAGAAUUGGGGUGGAGUAGUAGUACGUGUACA 812
Db 1511 TTCTTGAATAATTTGCAGACCTATCAGAAACGAATGGGGTGCAGATGCAACGATTTCAAGT 1570
Qy 813 GAAC 816
Db 1571 GACC 1574

RESULT 6
US-11-131-479-97
; Sequence 97, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 97
; LENGTH: 7798
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4766, Ligation of Seg7 into VR4762
US-11-131-479-97

Query Match 72.4%; Score 681.6; DB 12; Length 7798;
Best Local Similarity 70.7%; Pred. No. 3.4e-75;
Matches 554; Conservative 166; Mismatches 64; Indels 0; Gaps 0;

Qy 33 GCUCACUUCUGGCAGACUUAAGAUAGUUCUUAACCGAGUGCGAAACGUAACGUUCUCU 92
Db 6070 GATCAGATATCGAATTGCCACCACTAGAGCTTCTAACCAGGTGGAACGATGTTCTCT 6129
Qy 93 CUUAUACCCGUCAGGCCCCUCUAAAGCCGAGAGUCGCAAGAGUAGUAGUUCUUG 152
Db 6130 CTATCGTTCCATCAGGCCCCCTCAAAGCCGAAATCGCGCAGAGACTTGAAGATGTTCT 6189
Qy 153 CAGGGAAGAACACCGAUUCUUGAGUUCUUAUGGAAUUGGCUAAAGACAGACCAUUCUCU 212
Db 6190 CTGGGAAAAACACAGATCTTTGAGGCTCTCATGGAATGGCTAAAGACAGACCAATCTCT 6249
Qy 213 CACUCUCUGAACGAGGAAUUAAGAUUUGUUCUACGUCACCGUGCCAGUGCGAG 272
Db 6250 CACCTCTGACTAAGGGGATTTGGGGTTGTGTTCACGCTCACCGTCCCGAGTGGCGAG 6309
Qy 273 GACUGCAGCGUAGCAGCUCUUAUGCAAAUUGCCUUAUUGGCAAAUUGGUAACAACCAACCA 332
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Db 6310 GACTCAGCGTAGACGCTTTGTCCAAAATGCCCTCAATGGGAATGGGGATCCAAATAC 6369
Qy 333 UGGACAAAGCAGUUAACUGUAUAGGAAGCUCACAGAGGAGGAUAACAUUCCAUUGGGGCA 392
Db 6370 TGGACAGAGCAGTTAAACTATATAGAAAACCTTAAGAGGGAGATTACATTCATGGGGCA 6429
Qy 393 AAGAAUUCUCACUCAGUUAUUCUGUGUGCAUUGCCAGUUGUAUUGGGCCUCUAUACA 452
Db 6430 AAGAAATAGCACTCAGTTATTCTGCTGGTGCACTTGGCCAGTTGCAATGGGCCCTCATATA 6489
Qy 453 ACAGAAUGGGGCGUGUGACCAUGAAGUGGCAUUGGCGGUGUAUGUACCUUGAAC 512
Db 6490 ACAGAAUGGGGCGTAAACCACTGAAGTGGCTTTGGGCTTGTGTATGTGCAACATGTGAAC 6549
Qy 513 AGAUUGUGAUCCCGCAGCAUGGUCUAUAGGCAAAUGGUGACAAACCAACCAUUA 572
Db 6550 AGATTGCTGACTCCAGCAGCAGGTCTCATAGGCAAAATGGTGGAACCAATCCATTA 6609
Qy 573 UCAGACUAGAGAACAGAAUGGUUUUAGCCAGCACAUCACAGCUAAGGCUAUGGCAAAUGG 632
Db 6610 TAAGGCATAGAAACAGAAATGGTTTGGCCAGCACTACAGCTAAGGCTATGGAGCAATGG 6669
Qy 633 CUGAUCCAGUGAGCAAGCAGCAGGCGCAUGGAGGUUGUAGUCAGGCUAGGCAUUGG 692
Db 6670 CTGGATCAAGTGAGCAGGCGAGGCGCATGGAAATTTGCTAGTCAGGCGCAGGCAATGG 6729
Qy 693 UGCAAGCGAUGAGAACCAUUGGGACUCAUCCUAGCUCUAGCUGGUGUGAUAUUAUGAUC 752
Db 6730 TGCAGGCAATGAGAGCCATTGGGACTCATCTAGCTCCAGTGTGCTTAAAGATGATC 6789
Qy 753 UUCUUGAAAAUUGCAGGCGCUAUCAGAAACGAAUGGGGUGCAGUAGCAACCGUUCUACGU 812
Db 6790 TTCTTGAANAATTCGACACCTATCAGAACCAAGTGGGGGTGCAGATGCAACGATTCAGT 6849
Qy 813 GAAC 816
Db 6850 GACC 6853

RESULT 7
US-11-131-479-98/c
; Sequence 98, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; PRIOR FILING DATE: 2005-05-18
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 98
; LENGTH: 7798
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4767, Ligation of Inverted RSVseg7 into VR4762

US-11-131-479-98
Query Match 72.4%; Score 681.6; DB 12; Length 7798;
Best Local Similarity 70.7%; Pred. No. 3.4e-75;
Matches 554; Conservative 166; Mismatches 64; Indels 0; Gaps 0;

Qy 33 GCUACAUCUUUGGCGAGUUAAGAGUAGUUCUUAACCGAGUGCGAAACGUAACGUCUCU 92
Db 6745 GATCAGATATCGAATTCGCCCAACCATGAGCCTTCTTAACCGAGGTGCGAAACGATGTCTCT 6686

Qy 93 CUAUCAUCCGUGCAGGCCCCUCUCAAAGCCGAGAUUCGACAGAGACUUGAAGAUUCUUG 152
Db 6685 CTATCGTTCCATCAGGCCCCCTCAAAGCCGGAATCGCGACAGACTTGAAGATGCTTTG 6626
Qy 153 CAGGGAAGAACACACGAUCUUGAGUUCUUAUGGAUUGGCUUAAGAACAGAACCAUUCUGU 212
Db 6625 CTGGGAAAAACACAGATCTTGGGCTCTCATGGAAATGGCTAAAGAACAGAACCAATCTCTGT 6566
Qy 213 CACCUCUGACUUAAGGGGAUUUAGGAUUUUGUUCACGCUACCCGUGCCAGUGAGCGAG 272
Db 6565 CACCTCTGACTTAAGGGGATTTTGGGTTTGTGTTTTCAGCTCACCGTGCCTGAGCGAG 6506
Qy 273 GACUGCAGCGUAGACGCUUUCUCAAUUGCCUUAUUGGGAACCGGGAUCCAAUUAACA 332
Db 6505 GACTGACGCTAGACGCTTGTCCAAATGCCCTCAATGGGAATGGGATCCAAATAACA 6446
Qy 333 UGGAACAAGCAGUUUAAACUGUAUAGGAAGCUCUAAAGAGGAGGAUAACAUCUUCUUGGGGCA 392
Db 6445 TGGACAGAGCAGTTAAACTATATAGAAAACCTTAAGAGGGAGATTACATTCATGGGGCA 6386
Qy 393 AAGAAUUCUACUCAGUUAUUCUGUGGUGCAGUUGCAGUUGUAUUGGGCCUCAUUAACA 452
Db 6385 AAGAAATAGCACTCAGTTATTCTGCTGGTGCCTTGCAGTTGCATGGGCTCATATACA 6326
Qy 453 ACAGAAUGGGGCGUGUGACCAUCAGAGUGGCAUUGGCGCUUGUAUUGCAACUGUGAAC 512
Db 6325 ACAGAAUGGGGCGTGTAAACCACTGAGTGGCTTTGGCTGTATGTGCAACATGTGAC 6266
Qy 513 AGAUUGCUGACUCCAGCAGCUGGUCUUAUAGGCAAAUGGUGACAAACCAACCAUUA 572
Db 6265 AGATTGCTACTCCAGCAGCAGGTCTCATAGGCAAAATGGTGGCAACCAACCAATCCATTA 6206
Qy 573 UCAGACUAGNACAGAAUGUUUUUAGCCAGCAGCAGUAGGCUUAGGAGGCAUUGGAGCAUUGG 632
Db 6205 TAAGGCATAGAAACAGAAATGGTTTGGCCAGCACTACAGCTAAGGCTATGGAGCAAAATGG 6146
Qy 633 CUGGAUCGAGUGAGCAGCAGAGGCGCAUGAGGUUUGUAGUAGGCUAGGCAUAGGCAUUGG 692
Db 6145 CTGGATCAAGTGAGCAGGCGGAGGCCATGGNAATTTGCTAGTCAGGCGAGGCAATGG 6086
Qy 693 UGCAAGCAGUAGAAACCAUUGGAGCUCUACUAGCUCUAGCUGGUGUUGAAGAAUAGUAC 752
Db 6085 TGCAGGCAATGAGAGCCATTTGGGACTCATCTAGCTCAGTGTGCTTAAAGATGATC 6026
Qy 753 UUCUUGAAAAUUGCAGGCGCUUUCAGAAACGAAUGGGGUGCAGUAGGCUUUCUACGU 812
Db 6025 TTCTTGAANAATTTGCAGACCTATCAGAAACGAATGGGGGTGCAGATGCAACGATTCAGT 5966
Qy 813 GAAC 816
Db 5965 GACC 5962

RESULT 8
US-11-131-479-60
; Sequence 60, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3

Qy 476 GAAGGCGAUUUGGCCUGGUAUGUGGACCUUGAGCAAGAUUGUGGACUCCAGCAUUGG 535
Db 2072 GAAGTGGCCTTTGGCTGGTATGTGCAACATGTGAACAGAGATTGCTGACTCCAGCACAGG 2131
Qy 536 UCUCUAUGGCAAAUUGUGGACAAACCAACCAACCAUUAUCAGACAUAGAGAACAGAAUUGGU 595
Db 2132 TCTCATAGGCAAAATGGTGGCAACCAACCAATCCATTAATAGGCGATGAGAACAGAAATGGTT 2191
Qy 596 UUAAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUUGGCGUGAUCGAGUGAGCAAGCAGCA 655
Db 2192 TTGGCCAGCACTACAGCTAAGGCTATGGAGCAAAATGGCTGATCAAGTGAAGCAGCAGCG 2251
Qy 656 GAGGCCAUGGAGUUGUAGUCAGGCUAGGCAAAUUGGUGGCGAAGAGAGAACCAUUGGG 715
Db 2252 GAGGCCATGGAATTTGCTAGTCAGGCCAGGCAAAATGGTGCAGGCAATGAGAGCCATTGGG 2311
Qy 716 ACUCAUCCUAGCUCUAGGUGGUGUGAAGAAUUGAUCUUAUAGAAUUAUUGCAGGCCUUAU 775
Db 2312 ACTCATCTAGCTCAGTGTGCTTAAAGATGATCTTCTTGAANAATTTGCAGACCTAT 2371
Qy 776 CAGAAACGAUUGGGGUGGAGCAAGCAACGCUUUAAGUGAAC 816
Db 2372 CAGAAACGAATGGGGTGCAGATGCAACGATTCAAGTGACC 2412

RESULT 12

US-11-131-479-100
; Sequence 100, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; PRIOR FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 100
; LENGTH: 7798
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4769, Ligation of Inverted NP into VR4756
US-11-131-479-100

Query Match 72.3%; Score 681; DB 12; Length 7798;
Best Local Similarity 72.0%; Pred. No. 4,1e-75;
Matches 548; Conservative 163; Mismatches 50; Indels 0; Gaps 0;
Qy 56 AUGAGUCUUAACCGAGGUGGAAACGUAACGUUCUUAUCCGUGACGCCGCCUCC 115
Db 1652 ATGAGCCTTCTAAACCGAGGTGCAACGATGTCTCTCTATCTTCCATCAGGCCGCCCTC 1711
Qy 116 AAAGCCGAUGGCGACAGAGACUUAAGAUUGUUGGAGGAGAGAACCCGACUUGAG 175
Db 1712 AAAGCCGAATTCGCGACAGACTTGAAGATGTCTTTGCTGGGAAAAACACAGATCTTGAG 1771
Qy 176 GUUCUUAUGGAUGGCUAAAGCAAGACCAUCCUGUACCUUUAAGGGAUUUA 235
Db 1772 GCTCTCATGGATGGCTAAGACAAACACCAATCTCTGCTCTGACTTAAGGGATTTG 1831
Qy 236 GGAUUGUUAACGCUCAACCGUGCCAGUGAGCGAGGAGUAGCGUUAUGUC 295
Db 1832 GGGTTGTGTTACGCTCACCGTGCAGTGCAGGAGCTGCAGCGTAGACGCTTTGTC 1891
Qy 296 CAAAUGCCUUAUUGGNAACGGGNAUCCAAUAUAGGACAAAGCAAGAUUAACUGUAU 355

Db 1892 CAAAATGCCCTCAATGGGAATGGGATCCAAATAACATGACAGAGAGTTAACTATAT 1951
Qy 356 AGGAAGCUCUAAGAGGAGAUAAUUAUUGGGCCAAAGAAAUUAUCUACUCAGUUAUUCU 415
Db 1952 AGAAAACCTTAAGAGGAGATTACATTCATGGGGCCAAAGAAATAGCACTCAGTTATCT 2011
Qy 416 GCUGGUCACUUCGCCAGUUAUGGGCCUUAUAUACAAAGGAUGGGGGGUGUGACCAU 475
Db 2012 GCTGGTGCACTTCCAGTTGTCATGGGCCTCATATACAACAGAAATGGGGGCTGTAACCACT 2071
Qy 476 GAAGUGGCAUUGGCCUGGUAGUGCAACCGUGUAAACAGAUUCGUGACUCCAGCAUUGG 535
Db 2072 GAAGTGGCCTTTGGCCCTTGGTATGTGCAACATGTGAACAGATTGCTGACTCCAGCACAGG 2131
Qy 536 UCUCUAUGGCAAAUUGGUGAACCAACCAACCAACCAUUAUACAGAUAGAAACAGAAUUGGU 595
Db 2132 TCTCATAGGCAAAATGGTGGCAACCAACCAATCCATTAATAGGCATGAGAACAGAAATGGTT 2191
Qy 596 UUAAGCCAGCACUACAGCUAAGGCUAUGGAGCAAAUUGGUGGAGGAGGAGGAGCAGCA 655
Db 2192 TTGGCCAGCACTACAGCTAAGGCTATGGAGCAAAATGGCTGATCAAGTGAAGCAGGCG 2251
Qy 656 GAGGCCAUGGAGGUUGCUAGUCAGGCUAGGCAAAUUGGUGCAAGCAAGUAGAAACCAUUGG 715
Db 2252 GAGGCCATGGAATTTGCTAGTCAGGCAGGCAAAATGGTGCAGCAATGAGGCCATTGGG 2311
Qy 716 ACUCAUCCUAGCUCUAGGUGGUGUGUAGAAUUAUUGAUCUUAUAGAAUUAUUGCAGGCCUUAU 775
Db 2312 ACTCATCTAGCTCCAGTGTGCTTAAAGATGATCTTCTTGAANAATTTGCAGACCTAT 2371
Qy 776 CAGAAACGAUUGGGGUGGAGCAAGCAACGCUUUAAGUGAAC 816
Db 2372 CAGAAACGAATGGGGTGCAGATGCAACGATTCAAGTGACC 2412

RESULT 13

US-11-131-479-106
; Sequence 106, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; PRIOR FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 106
; LENGTH: 8442
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4775, Ligation of RSV RSeg7 into VR4762
US-11-131-479-106

Query Match 72.3%; Score 681; DB 12; Length 8442;
Best Local Similarity 72.0%; Pred. No. 4e-75;
Matches 548; Conservative 163; Mismatches 50; Indels 0; Gaps 0;
Qy 56 AUGAGUCUUAACCGAGGUGGAAACGUAACGUUCUUAUCCGUGACGCCGCCUCC 115
Db 6426 ATGAGCCTTCTAAACCGAGGTGCAACGATGTGCTCTCTCTATCTGTTCCATCAGGCCCTC 6485
Qy 116 AAAGCCGAUUGGCGACAGACUUAAGAUUGUUAAGAGAGGAGAAACACCGCAUUCUAG 175

Db 6486 AAAAGCCGAAATCGCCAGAGACTTGAAGATGTCTTTGCTGGGAAAAACACAGATCTTGAG 6545
Qy 176 GUUCUAGGAUGGCUAAAGACAAAGACCAUCCUGUACACUCUACUUAAGGGGAUUAU 235
Db 6546 GCTCTCATGGAATGGCTAAGACAGACAAATCTCTGTCACCTCTGACTAAGGGGATTITG 6605
Qy 236 GGAUUGUUGUUCACGCUACACCGUGCCGAGUGAGGAGGACUGCAGCGUAGACGCUUUGUC 295
Db 6606 GGGTTTGTGTTTTCAGCTCAGCGTCCAGTGCAGGAGGACTGCAGCGTAGACGCTTTGTC 6665
Qy 296 CAAAAGCCCUUAUUGGGAUCCGGGAUCCGGAUCCAAUAUAACAGGACAAAGACAGUUAACUGU 355
Db 6666 CAAAATGCCCTTATGGGAATGGGATCCAAATAACATGGACAGAGCTTTAAATATAT 6725
Qy 356 AGGAAGCUCAGAGGAGGAUAACAUUCCUAGGGGCCAAAGAAUUCUCACUACUUAUUCU 415
Db 6726 AGAAACTTAAAGAGGAGATTAATCTTCCATGGGGCCAAAGAAATAGCACTCAGTTATTTCT 6785
Qy 416 GUGUGGACUUGGCGAGUUGUAGGCGCTCUAUUAACAAAGAGUAGGGGCGUGUACCAU 475
Db 6786 GCTGTGCTTGGCTTGGCTTGGTATGTGCAATGGGCTCATATACAAAGAAATGGGGCTGTAACCACT 6845
Qy 476 GAAUGGCAUUGGCGUGUAGUUGUACCAUCCUGUAGAAAGAUUGUAGUUGUAGUUGG 535
Db 6846 GAAAGTGGCTTGGCTTGGTATGTGCAATGGGCTCATATACAAAGAAATGGGGCTGTAACCACT 6905
Qy 536 UCUAAGGCAUUGGUGAGCAACCAACCAUCCUAGGCGCAUUAUCAGACAGUAGAAAGUUGU 595
Db 6906 TCTCATAGGCAATGGTGGCAACCAATCTTAAATAGGCAATGGGCTGTAACCACT 6965
Qy 596 UAGGCGACACUACAGGCUAAGGCUAAGGAGCAUUGGCGUAGUAGUAGUAGUAGUAGUAG 655
Db 6966 TTGGCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGATCAAGTGAAGGAGGAGG 7025
Qy 656 GAGGCAUUGGAGUUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 715
Db 7026 GAGGCAUUGGAGUUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 7085
Qy 716 ACUACUAGGCUAGGCUAGGCUAGGCUAGGCUAGGCUAGGCUAGGCUAGGCUAGGCUAG 775
Db 7086 ACTCATCTAGCTCAGTGGCTGCTTAAAGATGATCTTCTTGAAGATGATCTTCTTGAAGAT 7145
Qy 776 CAGAAACGAAUUGGGGUGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 816
Db 7146 CAGAAACGAAUUGGGGUGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 7186

RESULT 14

US-11-131-479-107/c
; Sequence 107, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 107
; LENGTH: 8442
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4776, Ligation of Inverted RSV R Seg7 into VR4762
US-11-131-479-107

Query Match 72.3%; Score 681; DB 12; Length 8442;
Best Local Similarity 72.0%; Pred. No. 4e-75;
Matches 548; Conservative 163; Mismatches 50; Indels 0; Gaps 0;
Qy 56 AUGAGUUCUUAUCCGAGGUGGAAACGUAUGUUCUUAUCCGUGUAGGAGGAGGAGGAGG 115
Db 7033 ATGAGCCTTCTAAACGAGGTCGAAACGATATGTTCTCTATCTGTTCCATGAGGAGGAGG 6974
Qy 116 AAAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 175
Db 6973 AAAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6914
Qy 176 GUUCUAGGAAUUGGCUAAAGACAAAGACCAUCCUAGUACCAUCCUAGUACCAUCCUAGU 235
Db 6913 GCTCTCATGAGTGGCTAAGACAGAACCAATCTCTGTCACCTCTGACTAAGGGGATTITG 6854
Qy 236 GGAUUGUUGUACGCUACGUGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 295
Db 6853 GGGTTTGTGTTTTCAGCTCAGCGTCCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6794
Qy 296 CAAAAGCCCUUAUUGGGAUCCGGAUCCAAUAUAACAGGCAAGGAGGAGGAGGAGGAGGAG 355
Db 6793 CAAAATGCCCTCAATGGGAATGGGGATCCAAATAACATGGAGCAGCTTTAAATATAT 6734
Qy 356 AGGAAGCUCAGAGGAGGAUAACAUUCCUAGGGGCCAAAGAAUUCUCACUACUUAUUCU 415
Db 6733 AGAAACTTAAAGAGGAGATTAATCTTCCATGGGGCCAAAGAAATAGCACTCAGTTATTTCT 6674
Qy 416 GUGUGGACUUGGCGAGUUGUAGGCGCUCAUAUACCAAGAGGAGGAGGAGGAGGAGGAGG 475
Db 6673 GCTGTGCACTTGGCAGTTGCTGGGCTCATATACAAAGAAATGGGGCTGTAACCACT 6614
Qy 476 GAAUGGCAUUGGCGUGUAGUUGGCAUCCUGUAGAAAGAUUGUAGUAGUAGUAGUAGUAG 535
Db 6613 GAAAGTGGCTTGGCTGGTATGTGCAACATGTGAACAGATTTGCTGACTCCGAGCAGG 6554
Qy 536 UCUAAGGCAUUGGUGACAAACCAACCCACUUAUACAGACAGUAGAAAGUUGU 595
Db 6553 TCTCATAGGCAATGGTGGCAACCAACCAATCCATTATAGGCATGAGACAGATGTTTCT 6494
Qy 596 UAGGCGACACUACAGGCUAAGGCUAUGGAGCAAAUUGGCGUAGUAGUAGUAGUAGUAG 655
Db 6493 TTGGCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTGATCAAGTGAAGCAGGAGG 6434
Qy 656 GAGGCAUUGGAGUUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 715
Db 6433 GAGGCAUUGGAGUUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 6374
Qy 716 ACUACUAGGCUAGGCUAGGCUAGGCUAGGCUAGGCUAGGCUAGGCUAGGCUAGGCUAG 775
Db 6373 ACTCATCTAGCTCAGTGGCTGCTTAAAGATGATCTTCTTGAAGATGATCTTCTTGAAGAT 6314
Qy 776 CAGAAACGAAUUGGGGUGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 816
Db 6313 CAGAAACGAAUUGGGGUGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 6273

RESULT 15

US-11-131-479-104
; Sequence 104, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18

; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 104
; LENGTH: 8450
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4773, Ligation of RSV RNP into VR4756
US-11-131-479-104

Query Match		72.3%;	Score 681;	DB 12;	Length 8450;
Best local Similarity		72.0%;	Pred. No. 4e-75;		
Matches 548;		Conservative 163;	Mismatches 50;	Indels 0;	Gaps 0;
Qy	56	AUGAGUCUUCUUAACCGAGGUCGAAACGUACGUUCUCUUAUCCCGUCAGGCGCCUC	115		
Db	1652	ATGAGCCTTCTAACCGAGGTGAAACGTAATGTTCTCTATCGTTCCATCAGGCCCCCTC	1711		
Qy	116	AAAGCCGAGUUCGACAGAGACUUGAAGAUUCUUGCAGGGAGAAACACCGAUUUGAG	175		
Db	1712	AAAGCCGAAATCGCGCAGAGACTTGAAGATGCTTTGCTGGGAAAAACACAGATCTTGAG	1771		
Qy	176	GUUCUCAUGGAUUGGCUAAGACAAAGACCAUCCUGUCUCCUCUGACUAGGGGAUUUA	235		
Db	1772	GCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACTCTGACTAAGGGGATTTTG	1831		
Qy	236	GGAUUUGUUCACGUCACCGUCGCCAGUGCGGAGACUGCAGCGUAGACGCUUUGUC	295		
Db	1832	GGGTTTGTTCAGCTCACCCTGCCAGTGAGCGAGGACTGCGAGCGTAGCGCTTTGTC	1891		
Qy	296	CAAAUUGCCCUUUAUGGGAACGGGGUCCAAAUAAACAUGGACAAAGCAUUUAAACUGUAU	355		
Db	1892	CAAAATGCCCTCAATGGGAATGGGATCCAAATAACATGACAGAGCAGTTAAACTATAT	1951		
Qy	356	AGGAAGCUCAAGAGGGAUAACAUCUCCAUUGGGGCCAAAGAAUUCACUCAGUUUUCU	415		
Db	1952	AGAAAACTTAAAGAGGGAGATTACATTCCATGGGGGCCAAAGAAATAGCACTCAGTTATCT	2011		
Qy	416	GCUGGUCACUUGCAGUUAUGGGCCUUAUACACAGGAGUUGGGGCGUGUACCAU	475		
Db	2012	GCTGGTGACCTTGCAGTTGCTGGGCTCATATACAACAGATGGGGGCTGTAAACCACT	2071		
Qy	476	GAAUGGCAUUGGCCUUGUUGUUGCAACUUGGAAACAGAUUUGCUCUCCAGAUCCG	535		
Db	2072	GAAGTGGCTTTGGCTGTGTATGTCAACATGTGAACAGATTGCTGACTCCAGCACAGG	2131		
Qy	536	UCUUAUGGCAUUGGUGACAACAACCAACCCACUUAUCAGACAGAGAAUGGUU	595		
Db	2132	TCTCATAGGCAAAATGGTGGCAACCAACCAATCCATTAAATAGGCATGAGAACAGAAATGGTT	2191		
Qy	596	UUAGCCAGCACUACAGCUAAGCUAUGGAGCAAAUUGGUGGAGUAGGAGCAAGCAGCA	655		
Db	2192	TTGGCCAGCACTACAGCTAAGGCTATGGAGCANAATGGCTGGATCAAGTGACAGGCGCG	2251		
Qy	656	GAGGCCAUGGAGGUUGUAGUCAGCUGAGCAAAUUGGUGCAAGCGAUGAGAACCAUUGGG	715		
Db	2252	GAGGCCATGGAAATTTGCTAGTCAGGCCAGGCAATGGTGCAGGCAATGAGAGCCATTGGG	2311		
Qy	716	ACUUAUCCUAGCUCGUGGUGUUAAGAAUUAUGAUUUCUUGAAAUUUUUCAGGCCUUAU	775		
Db	2312	ACTCATCTAGCTCAGTGGTCTAAAGATGATCTCTTTGAAAAATTTGCAGACCTAT	2371		
Qy	776	CAGAAACGAUUGGGGUGCAGUACGACGGUUCAGUGAAC	816		
Db	2372	CAGAAACGAATGGGGGTGCAGATGCACGATTCAGTGACC	2412		

Search completed: March 21, 2006, 01:31:34
Job time : 430.258 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2006, 23:02:13 ; Search time 190.994 Seconds
(without alignments)
8767.110 Million cell updates/sec

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Perfect score: 942
Sequence: 1 gcuuucuuuuuugcagaag.....aaaaaaaaaaaaaaaaaaaa 942

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 130357 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents NA.*
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8: /cgn2_6/ptodata/1/ina/RE_COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488.8	51.9	4023	3	US-08-809-513A-8
2	487.4	51.7	1023	3	US-09-506-286B-1
3	487.4	51.7	1023	3	US-09-762-861B-1
4	487.4	51.7	1023	3	US-10-065-133A-1
5	487.4	51.7	1023	3	US-10-434-811A-1
6	486.6	51.7	6802	3	US-08-809-513A-6
7	484.6	51.4	1023	3	US-09-506-286B-4
8	484.6	51.4	1023	3	US-09-762-861B-4
9	484.6	51.4	1023	3	US-10-065-133A-4
10	484.6	51.4	1023	3	US-10-434-811A-4
11	477.4	50.7	816	3	US-09-311-784A-13
12	477.2	50.7	756	3	US-09-506-286B-3
13	477.2	50.7	756	3	US-09-762-861B-3
14	477.2	50.7	756	3	US-10-065-133A-3
15	477.2	50.7	756	3	US-10-434-811A-3
16	474.4	50.4	756	3	US-09-506-286B-6
17	474.4	50.4	756	3	US-09-762-861B-6
18	474.4	50.4	756	3	US-10-065-133A-6
19	474.4	50.4	756	3	US-10-434-811A-6
20	473.4	50.3	1027	6	PCT-US95-12357A-3
21	79.4	8.4	290	3	US-10-131-827-8418
22	79.4	8.4	1069	3	US-09-372-422A-7
23	77.6	8.2	1097	3	US-09-832-129-21
24	76.8	8.2	569	3	US-09-461-325-44

25	76.8	8.2	569	3	US-10-012-542-44	Sequence 44, Appl
26	76.8	8.2	569	3	US-10-115-123-44	Sequence 44, Appl
27	76.8	8.2	3080	3	US-09-099-041A-25	Sequence 25, Appl
28	76.8	8.2	3080	3	US-09-245-281-25	Sequence 25, Appl
29	76.8	8.2	3080	3	US-09-207-359B-25	Sequence 25, Appl
30	76.8	8.2	3080	3	US-09-340-520A-25	Sequence 25, Appl
31	76.8	8.2	3080	3	US-09-865-364-25	Sequence 25, Appl
32	76.8	8.2	3080	3	US-09-728-721-25	Sequence 25, Appl
33	76	8.1	1733	3	US-09-073-569-1	Sequence 1, Appl
34	75.8	8.0	990	3	US-09-800-729-79	Sequence 79, Appl
35	75.8	8.0	1934	3	US-08-776-844-1	Sequence 1, Appl
36	75.8	8.0	1934	3	US-09-909-325-1	Sequence 1, Appl
37	75.8	8.0	1934	3	US-09-909-326-1	Sequence 212, App
38	75.8	8.0	1985	3	US-09-907-794A-212	Sequence 212, App
39	75.8	8.0	1985	3	US-09-905-125A-212	Sequence 212, App
40	75.8	8.0	1985	3	US-09-902-775A-212	Sequence 212, App
41	75.8	8.0	1985	3	US-09-906-700-212	Sequence 212, App
42	75.8	8.0	1985	3	US-09-903-603A-212	Sequence 212, App
43	75.8	8.0	1985	3	US-09-904-520A-212	Sequence 212, App
44	75.8	8.0	1985	3	US-09-909-064-212	Sequence 212, App
45	75.8	8.0	1985	3	US-09-905-381A-212	Sequence 212, App

ALIGNMENTS

RESULT 1

US-08-809-513A-8
; Sequence 8, Application US/08809513A
; Patent No. 6524588
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
; TITLE OF INVENTION: Method
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NORRIS McLAUGHLIN & MARCUS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Gateway Pentium II
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,513A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03663
; FILING DATE: 18-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94115505.3
; FILING DATE: 30-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Hobom 9832-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4023 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

Qy	526	CCAGCACGCGACGACACAGGCAGAUUGUGACACACACCAACCCCUCAUGACGACGAGAA	585
Db	495	CCAGCATCGATCTCCACAGGCAGATGGTGACAAACCAACCCATTTAATCAGATCATGAAAA	554
Qy	586	CAGGAUGGUGUGUGGCCAGACCAACCGCCAGGCCAUGGAGCAGAUUGCGCGGACGACGCA	645
Db	555	CAGAAATGGTATTAGCCAGTACCAACGGCTAAAGCCATGGAGCAGATGGCAGGGTCGAGTCA	614
Qy	646	CGAGGCGCGCGAGGCCAUGGAGGUGGCCAGCCAGGCACAGGCAUGUGUGUCAGGCCAUGAG	705
Db	615	CGAGGCAGCAGAGGCCATGGAGGTTGCTAGTAAGGCTAGGCAGATGGTTCAGGCAATGAG	674
Qy	706	GACCAUCGCGCACCAACCCACAGCAGCGCGCGCGCUGAAGAACGACCUUGUCGAGAACCU	765
Db	675	AACCATTTGGGACCAACCCCTAGCTCAGTGC CGGTTTGAAGATGATCTCCTTTGAAATTT	734
Qy	766	CGAGGCGCUAACAGAAAGCGCAUGGCGGUGCAGAUAGCAGCGCUUCAAGUGAAC	816
Db	735	CGAGGCGCTACAGAAAAAGGATGGGAGTGCAATGCGAGCATTCAGTGTATC	785

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US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023

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Query Match	Score	DB 3	Length
Best Local Similarity	51.7%	487.4	1023
Matches 501: Conservative	65.0%	Pred. No. 6.8e-74	
Matches 501: Conservative	93	Mismatches 177	Indels 0
			Gaps 0

Qy	46	AGAUUCUAAAGAUGAGCGCCUGCUGACCCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCCCAG	105
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Qy	106	CGGCCCCCUGAAGGCCGAGAGUCGCCCCAGAGGCCUGGAGGAGCGUUVUCCGCCGCCAGNAACAC	165
Dp	75	AGGCCCCCTCAAGACCGAGATCGGCAGAGACTTGAAGATGTCCTTGCAGGGGAAGAACAC	134

Qy	166	CGACTUGGAGGUCUGAUGGAGUGGCTUGAAGACAAGGGCCCAUCCUGAGCCCCCUGACCAA	225
Dp	135	CGACTCTTGAGGCACTCATGGAATGGCTAAAGACAAGACCAATCTGTGACCTCTGACTAA	194

Qy	226	GGGCAUCCUGGGCUUUGUUUUAACCTTUGACCGUGCCCAAGGAGCGCGGCCUUCAGCGCCG	285
Db	195	AGGGATTTTAGAGTTTCGTATTACAGCTCACCGTGCCTCCTGAGCGAGGACTGCAGCGTAG	254

Query Match 51.7%; Score 487.4; DB 3; Length 1023;
Best Local Similarity 65.0%; Pred. No. 6.8e-74;
Matches 501; Conservative 93; Mismatches 177; Indels 0; Gaps 0

Qy 46 AGAUCUAAAGAUAGAGCCUGCUGACCGGAGGUGGAGACCTUACGUGCUGAGCAUCAUCCCCAG 105

Dd 15 ATATTTTAAAGATGAGTCTTCTGACCGAGGTGCGAAACGTGAGTCTCTCTATCTGATCCATC 74

Qy	106	CGGGCCCCUGAAGCGCGAGAUCCGCCAGAGGCTUGAGGACGUGUUCGCCGGCAAGAAC	165
Db <td>75 <td>AGGCGCCCTCAAGAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTCAGGGGAAGAAC <td>134</td> </td></td>	75 <td>AGGCGCCCTCAAGAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTCAGGGGAAGAAC <td>134</td> </td>	AGGCGCCCTCAAGAGCCGAGATCGCGCAGAGACTTGAAGATGTCTTTCAGGGGAAGAAC <td>134</td>	134

Qy	166	CGACCUGGAGGUCUGAUGGAGUGGCTUGAAGACGAGGCCAUCUCGAGGCCCCUGACCAA	225
Db <td>135 <td>CGATCTTGAGGCACCTCATGGAATGGCTAAAGACAAGACCAATCTGTGACCTCTGACTTAA <td>194</td> </td></td>	135 <td>CGATCTTGAGGCACCTCATGGAATGGCTAAAGACAAGACCAATCTGTGACCTCTGACTTAA <td>194</td> </td>	CGATCTTGAGGCACCTCATGGAATGGCTAAAGACAAGACCAATCTGTGACCTCTGACTTAA <td>194</td>	194

Qy	226	GGGCAUCCUGGGCUUCGUGUUCACCCUGACCGUGCCACGAGCGCGGCCUUGCAGCGCG	285
Db	195	AGGGATTTTAGGATTCGTTATTCAGCTCACCGTCCCACTGAGCGGAGGACTCGACGCTAG	254

Qy	286	CCGCUUCUGCAGNAACGCCCUAGAACGGCGAACCGCGACCCCAACAACAUGGACAAGGCCGU	345
Db	255	ACGCTTTTGC AAAATGCCCTTACTGTGAAACGGAGATCAAAACAACATCGACACAGACGAT	314

Qy 346 GAGCTGUAACAGGAAGCTUGAAGAGGGAGAGUACCTUUCACGGCGCCACGAGAGAUACGCTU 405
Db 315 AAAATGTGACAGGAAGCTTTAAAGAGAGAAATAACAATTCCTATGGGCAAGAGAGGTGGCACT 374

Qy	406	GAGCUCACAGCGCCGGCGGCCUUGGCGCAGUCGCAUGGCCUGAUCUAACAACGAGGAUGGGCGC	465
Db	375	CAGCTATTTCACGTGTGCATAGCCAGCTCATGGGACTCATATAACAAGAATGGGAAC	434

Qy	466	CGUGACCAACCGAGGUGCCUUCGGCTTUGGUGGCCCAACGUGCAGACAGCGGCAGAG	525
Db	435	TGTGACAACCGAAGTGGCATTTTGCCCTGGTATGCGCCAATGTGAACAGATCGCTGATT	494

Db 481 TCTCAGCGCAGATGGTGACAAACCAACCAACCAATTAATCAGACATGAAACAGAAATGGTA 540
Qy 596 CUGGCCAGCACACCGCCCAAGCCCAUGGAGGAGUAGGCGCGGCGAGCGAGCGCGCCG 655
Db 541 TTAGCCAGTACACCGCTAAAGCCATGAGCAGATGGCAGGCTGAGTGCAGGAGCA 600
Qy 656 GAGGCCAUGGAGGCGCCAGCCAGGCGAGGAGUAGGCGAGGCGAGGAGGAGGAGGAGG 715
Db 601 GAGGCCATGGAGTTGCTAGTAAGGCTAGGCGAGATGGTTCAGGCAATGAGAACCATTTGG 660
Qy 716 ACCCAACCCAGCAGCGCGCGCCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 775
Db 661 ACCCAACCCAGTCTCAGTGCAGGCTTTGAAAGATGATCTCTTGAATAATTTGAGGCTTAC 720
Qy 776 CAGAGCCCAUGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 811
Db 721 CAGAAACGGATGGGAGTGCAATGACGCGATTCAAG 756

RESULT 13
US-09-762-861B-3
; Sequence 3, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
; CURRENT APPLICATION NUMBER: US/09762, 861B
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133, 921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-762-861B-3

Query Match 50.7%; Score 477.2; DB 3; Length 756;
Best Local Similarity 65.1%; Pred. No. 3.5e-72;
Matches 492; Conservative 90; Mismatches 174; Indels 0; Gaps 0;

Qy 56 AUGAGCCUGCUGACCGAGGUGGAGACCUAGCUGCUGAGCAUCCCGAGCGGCCCGCUG 115
Db 1 ATGAGTCTTCTGACCGAGGTGCAAACTGATCTCTCTATCGTACCATAGGCGCCCTC 60

Qy 116 AAGGCCGAGUAGCGCCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 175
Db 61 AAAGCCGAGATCGCGAGAGACTTGAAGATGTCTTTGAGGAGGAGGAGGAGGAGGAGGAG 120

Qy 176 GUGCUGAUGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 235
Db 121 GCATCTCATGGAATGGCTAAAGACCAAGCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180

Qy 236 GGUUUGUUGUACCCUGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 295
Db 181 GGATTCGTATTTCAGCTCACCCTGCCAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240

Qy 296 CAGAAACCGCCUAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 355
Db 241 CAHAATGCCCTTAGTGGAAACGGAGATCCAAACCAACATGGACAGGAGGAGGAGGAGGAG 300

Qy 356 AGGAAGCUGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 415
Db 301 AGGAAGCTTAAAGAGAGAAATAACATCTTCATGGGGCAAAAGAGGAGGAGGAGGAGGAGG 360

Qy 416 GCCCGCGCCUGGCGCAGCUGCAUGGCGCUGAUCUACAAACAGAGUAGGCGCGGAGCACACC 475
Db 361 ACTGCTGCACTAGCCAGCTGCTGGACTCATATACAACAGAAATGGGAATGTGACAACC 420

Qy 476 GAGGCGCCTUUGGCGCUGGUGUGCGCCACCUAGCAGGAGGAGGAGGAGGAGGAGGAGGAG 535
Db 421 GAAGTGGCATTTGGCTGGTATGCGCCACATGTGAACAGATCGCTGATTTCCAGCATCGA 480

Qy 536 AGCCACAGGCGAGUAGGUGGAGCACCACCAACCCCGCUGAUCAGGCGACGAGAACGAGUGG 595
Db 481 TCTCAGGCGAGATGGTGACAAACCAACCAACCCATTATCAGACATGAAACAGAAATGGTA 540

Qy 596 CUGGCCAGCAGCACCGCCCAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 655
Db 541 TTAGCCAGTACCAACCGGCTAAAGCCATGAGCAGATGGCAGGCTGAGTGCAGGAGGAGCA 600

Qy 656 GAGGCCAUGGAGGUGGCGCAGCGCCAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 715
Db 601 GAGGCCATGGAGGTTGCTAGTAAGGCTAGGCGAGATGGTTCAGGCAATGAGAACCATTTGG 660

Qy 716 ACCCAACCCAGCAGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 775
Db 661 ACCCAACCCAGTCTCAGTGCAGGCTTTGAAAGATGATCTCTTGAATAATTTGAGGCTTAC 720

Qy 776 CAGAAACGGATGGGAGTGCAATGACGCGATTCAAG 811
Db 721 CAGAAACGGATGGGAGTGCAATGACGCGATTCAAG 756

RESULT 14
US-10-065-133A-3
; Sequence 3, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065, 133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133, 921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-3

Query Match 50.7%; Score 477.2; DB 3; Length 756;
Best Local Similarity 65.1%; Pred. No. 3.5e-72;
Matches 492; Conservative 90; Mismatches 174; Indels 0; Gaps 0;

Qy 56 AUGAGCCUGCUGACCGAGGUGGAGACCUAGCUGCUGAGCAUCCCGAGCGGCCCGCUG 115
Db 1 ATGAGTCTTCTGACCGAGGTGCAAACTGATCTCTCTATCGTACCATAGGCGCCCTC 60

Qy 116 AAGGCCGAGUAGCGCCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 175
Db 61 AAAGCCGAGATCGCGAGAGACTTGAAGATGTCTTTGAGGAGGAGGAGGAGGAGGAGGAG 120

Qy 176 GUGCUGAUGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 235
Db 121 GCATCTCATGGAATGGCTAAAGACCAAGCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180

Qy 236 GGUUUGUUGUACCCUGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 295
Db 181 GGATTCGTATTTCAGCTCACCCTGCCAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240

Qy 296 CAGAAACCGCCUAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 355

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Db      241  CAAAATGCCCTTAGTGGAAACGGAGATCCAAACACATGGACAGAGCAGTAAACCTGTAC 300
Qy      356  AGGAAGCUGAAGAGGAGAUCAACCUUCCACGGCCCAAGGAGAGAUCAAGCCUGAGCUACAGC 415
Db      301  AGGAAGCTTAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCC 360
Qy      416  GCGGCGCCUUGGCGAGCUGCAUGGCGCCUGAUCAACAAAGGAUGGGCGGUGAACCAACC 475
Db      361  ACTGGTGCATAGCCAGCTGCATGGGACTCATATACAAACAGAAATGGGAACCTGTGACAACC 420
Qy      476  GAGGUGGCCUUGCGGUGUGUGCGCCACCUUGCGAGCAGAUUGCGGACAGCCAGCACGCC 535
Db      421  GAAGTGGCATTTGGCCCTGGTATGGCTAGGCTAGGCAGATGGTTCGATGATCCAGCATCGA 480
Qy      536  AGCCACAGGAGAUUGGAGCACCACCAACCCCUUGAUCAAGGACGAGAGCAGAGAUUGUG 595
Db      481  TCTCACAGGCAGATGGTGACAAACCAACCCATTATCAGACATGAACAGAAATGGTA 540
Qy      596  CUGGCCAGCACCAACCGGCAAGGCCAUGAGCAGAUUGGCGGCGACGAGCAGGCGGCC 655
Db      541  TTAGCCAGTACCAACGGCTAAAGCCATGGAGCAGATGGCGGTTCGAGTGAGCAGGCAGCA 600
Qy      656  GAGGCCAUGGAGGUGGCGAGCCAGCGCAGGAGAUUGGCGGCAUGAGGAGCAACCAUGGC 715
Db      601  GAGGCCATGGAGGTGTCTAGTAAGGCTAGGCAGATGGTTCGATGATGAGAAACCATTTGGG 660
Qy      716  ACCCACCCAGCAGCAGCGCGCGCCUGAAGAACGACCUUGUGGAGAACCUUGCAGGCCUAC 775
Db      661  ACCCACCTAGCTCCAGTGCCTGTTGAAGATGATCTCCTTGAATAATTTGCAGGCCCTAC 720
Qy      776  CAGAAGCGCAUGGCGUGAGAUAGCAGCGCUUCAAG 811
Db      721  CAGAAGCGGATGGGAGTGCAATGCAGCGATTCAAG 756
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RESULT 15

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US-10-434-811A-3
; Sequence 3, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EO-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10434,811A
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-434-811A-3
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Query Match      50.7%; Score 477.2; DB 3; Length 756;
Best Local Similarity 65.1%; Pred. No. 3.5e-72;
Matches 492; Conservative 90; Mismatches 174; Indels 0; Gaps 0;

Qy      56  AUGAGCUGUGCAGCGGAGGAGACCUACGUGUGAGAUCAUCCCGAGCGGCCCCUG 115
Db      1  ATGAGTCTTTCGACCGGAGGTGGAACGTCACGTTCTCTATCGTACCATCAGGCCCCCTC 60
Qy     116  AAGGCCGAGAUUGCCCGAGGCGUGGAGGACGUGUUGCGCGGCAAGAAACACCGACCUAGG 175
Db      61  AAAGCCGAGATCGCGCAGAGACTTGAAGATGCTTTGCGAGGGAAGAACACCGCATCTTGAG 120
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Qy      176  GUUCUGAUGGAGUGGCUGRAGACAGGCCCAUCCUGAGCCCCCUGACRAGGGAUCCUG 235
Db     121  GCATCTATGAATGGGTAAAGACAAGACCAATCCTGTCACTCTGACTAAAGGATTTTA 180
Qy     236  GGUUGUGUUCACUCCUGACCGUGCCAGCGAGCGGGCCUGCAGCGCCCGCCGCUUGUG 295
Db     181  GGATTGGTATTACGCTCACCGTGCCAGTGAGCGGAGGACTGCAGCGGTAGACGCTTTGTC 240
Qy     296  CAGAACCCCGUGAACCGGCAACCGCGACCCCAACAAUAGCAAGGCGGUGAAGCUGUAC 355
Db     241  CAAAATGCCCTTAGTGGAAACCGGAGATCCAAACAAACATGACAGAGCAGTAAACCTGTAC 300
Qy     356  AGGAAGCUGAAGGAGGAGAUCAACCUUGCGGCGCAAGGAGAUCAAGCCUGAGCUACAGC 415
Db     301  AGGAAGCTTAAAGAGAAATAACATTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCC 360
Qy     416  GCGGCGCCCGUGGCCAGCUGCGGCGUGAUCAACAAAGGAGUGGCGCGGUGACCAACC 475
Db     361  ACTGGTGCATAGCCAGCTGCATGGGACTCATATACACAGAAATGGGAACCTGTGACAACC 420
Qy     476  GAGGUGGCCUUGCGGCGUGUGUGCGGCACCUUGCGAGCAGAUUGCGCGGACAGCCAGCCGC 535
Db     421  GAAAGTGGCATTTGGCCCTGGTATGGCGCACATGTGTAACAGATCGCTGATTTCCAGCATCGA 480
Qy     536  AGCCACAGGAGAUUGGUGACCAACCCCUUGAUCAAGGACGAGCAACAGAAACAGAUUGUG 595
Db     481  TCTCACAGGCAGATGGTGACAAACCAACCCATTATCAGACATGAACAGAAATGGTA 540
Qy     596  CUGGCCAGCACCAACCGGCAAGGCCAUGGAGCAGAUUGGCGGCGAGCAGCGAGCGGCCGCC 655
Db     541  TTAGCCAGTACCAACGGCTAAAGCCATGGAGCAGATGGCAGGGTTCGAGTGAGCAGGCAGCA 600
Qy     656  GAGGCCAUGGAGUGGCGCAGCCAGCGCAGGCGAGCAGAUUGGUGAGCGCAUAGAGGACCAUUGCGC 715
Db     601  GAGGCCATGGAGGTGTCTAGTAAGGCTAGGCAGATGGTTCGATGATGAGAAACCATTTGGG 660
Qy     716  ACCCACCCAGCAGCAGCGCGCGCCUGAAGAACGACCUUGUGGAGAACCUUGCAGGCCUAC 775
Db     661  ACCCACCTAGCTCCAGTGCCTGTTGAAGATGATCTCCTTGAATAATTTGCAGGCCCTAC 720
Qy     776  CAGAAGCGCAUGGCGUGAGAUAGCAGCGCUUCAAG 811
Db     721  CAGAAGCGGATGGGAGTGCAATGCAGCGATTCAAG 756
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Search completed: March 20, 2006, 23:50:27

Job time : 192.994 secs

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OM nucleic - nucleic search, using sw model

Run on: March 20, 2006, 23:29:50 ; Search time 925.936 Seconds
(without alignments)
8412.838 Million cell updates/sec

Title: US-10-729-830-6
Perfect score: 942
Sequence: 1 gcuugucuuuuugcagaag.....aaaaaaaaaaaaaaaaaaaaa 942

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413469005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:*
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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	942	100.0	942	8	US-10-729-830-6
2	884	93.8	1011	8	US-10-729-830-7
3	775	82.3	775	8	US-10-729-830-3
4	762	80.9	844	8	US-10-729-830-4
5	666.8	70.8	942	8	US-10-729-830-5
6	498.8	53.0	774	8	US-10-729-830-1
7	497	52.8	986	8	US-10-866-484-9
8	489.4	52.0	1027	6	US-10-177-390-31
9	487.8	51.8	1027	8	US-10-855-875-5
10	487.4	51.7	1023	6	US-10-065-133A-1
11	487.4	51.7	1023	7	US-10-434-811A-1
12	487.4	51.7	1023	7	US-10-734-373-1
13	487.4	51.7	1023	8	US-10-872-014-1
14	484.6	51.4	1023	6	US-10-065-133A-4
15	484.6	51.4	1023	7	US-10-434-811A-4
16	484.6	51.4	1023	7	US-10-734-373-4
17	484.6	51.4	1023	8	US-10-872-014-4
18	477.4	50.7	816	6	US-10-371-525-13
19	477.4	50.7	816	6	US-10-371-069-13
20	477.4	50.7	816	6	US-10-371-645-13
21	477.4	50.7	816	6	US-10-371-260-13
22	477.2	50.7	756	6	US-10-065-133A-3
23	477.2	50.7	756	7	US-10-434-811A-3

24	477.2	50.7	756	7	US-10-734-373-3	Sequence 3, Appli
25	477.2	50.7	756	8	US-10-872-014-3	Sequence 3, Appli
26	474.6	50.4	1002	3	US-09-747-335-3	Sequence 3, Appli
27	474.6	50.4	1002	7	US-10-435-723A-3	Sequence 3, Appli
28	474.4	50.4	756	6	US-10-065-133A-6	Sequence 6, Appli
29	474.4	50.4	756	7	US-10-434-811A-6	Sequence 6, Appli
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31	474.4	50.4	756	8	US-10-872-014-6	Sequence 6, Appli
32	473.4	50.3	1027	7	US-10-381-530-7	Sequence 7, Appli
33	472.6	50.2	759	8	US-10-617-569-3	Sequence 3, Appli
34	88.8	9.4	1476	3	US-09-374-046A-83	Sequence 83, Appli
35	88.8	9.4	1476	7	US-10-616-263-83	Sequence 83, Appli
C 36	84.2	8.9	573	7	US-10-424-599-135848	Sequence 135848,
C 37	83.4	8.9	362	8	US-10-425-115-68338	Sequence 68338, A
C 38	83	8.8	598	7	US-10-021-323-11423	Sequence 11423, A
C 39	82.8	8.8	510	7	US-10-437-963-1928	Sequence 1928, Ap
C 40	82.6	8.8	374	7	US-10-437-963-32121	Sequence 32121, A
C 41	82	8.7	405	8	US-10-425-115-76344	Sequence 76344, A
C 42	82	8.7	554	7	US-10-021-323-4489	Sequence 4489, Ap
C 43	82	8.7	1714	8	US-10-425-115-170894	Sequence 170894,
C 44	81.6	8.7	559	7	US-10-021-323-14094	Sequence 14094, A
C 45	81.6	8.7	585	8	US-10-425-115-169902	Sequence 169902,

ALIGNMENTS

RESULT 1
US-10-729-830-6
; Sequence 6, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA with increased G/C-content and
; OTHER INFORMATION: stabilisation sequences
; FEATURE:
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
; OTHER INFORMATION: respectively.
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
; OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-6

Query Match 100.0%; Score 942; DB 8; Length 942;
Best Local Similarity 100.0%; Pred. No. 4.5e-182;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GCUGUUCUUUUUGCAGAACUCAGAAUAAACGCUCUAACUUGGCGAGAUAAAGUAG 60
Db	1	GCUGUUCUUUUUGCAGAACUCAGAAUAAACGCUCUAACUUGGCGAGAUAAAGUAG 60
Qy	61	CCUGUGACCGAGGUGGAGACCUACUGUGGAGCAUCAUCCCCCGCGCCCCCUAGAGGC 120
Db	61	CCUGUGACCGAGGUGGAGACCUACUGUGGAGCAUCAUCCCCCGCGCCCCCUAGAGGC 120

[illegible]

RESULT 2

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US-10-729-830-7
: Sequence 7, Application US/10729830
: Publication No. US20050032730A1
: GENERAL INFORMATION:
: APPLICANT: Von der Muelbe, Florian
: APPLICANT: Hoerr, Ingmar
: APPLICANT: Pascolo, Steve
: TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
: FILE OF INVENTION: optimised for translation in its coding regions
: FILE REFERENCE: 2793-1-001pCT/CIP
: CURRENT APPLICATION NUMBER: US/10/729,830
: CURRENT FILING DATE: 2003-12-05
: PRIOR APPLICATION NUMBER: PCT/EP02/06180
: PRIOR FILING DATE: 2002-06-05
: NUMBER OF SEQ ID NOS: 13

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1011
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA coding for secreted form with
; OTHER INFORMATION: increased G/C-content and stabilisation sequences
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
; OTHER INFORMATION: codon: uga (nucleotides 881 to 883)
US-10-729-830-7

Query Match          93.8%;   Score 884;   DB 8;   Length 1011;
Best Local Similarity 100.0%;   Pred. No. 2,9e-170;
Matches 884;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY 59 AGCCUGCUGACCGAGGUGGAGACUACGUCGUGAGCAUCAUCCCCAGCGGCCCCCUAAG 118
   |||
Db 128 AGCCUGCUGACCGAGGUGGAGACUACGUCGUGAGCAUCAUCCCCAGCGGCCCCCUAAG 187

QY 119 GCCGAGAUCCGCNAGAGCTUGGAGGAGCGUUCGCGCGCAAGACACCCGACCTUGGAGGUG 178
   |||
Db 188 GCCGAGAUCCGCNAGAGCTUGGAGGAGCGUUCGCGCGCAAGACACCCGACCTUGGAGGUG 247

QY 179 CUGAUGGAGUGGCGUGAAGACACAGCGCCCAUCUCUGAGCCCCUGACGCGCCCGCUCUGUGCAG 238
   |||
Db 248 CUGAUGGAGUGGCGUGAAGACACAGCGCCCAUCUCUGAGCCCCUGACGCGCGCCCGCUCUGUGCAG 307

QY 239 UUCGUGUUCACCCUGACCGUGCCGACGAGCGCGGCGCUGCAGCGCCCGCUCUGUGCAG 298
   |||
Db 308 UUCGUGUUCACCCUGACCGUGCCGACGAGCGCGGCGCUGCAGCGCCCGCUCUGUGCAG 367

QY 299 AACGCCUCUGAAACGCAACGCGGACCCCAAACAACUGACACAGCCCGUGAGCUGUACAGG 358
   |||
Db 368 AACGCCUCUGAAACGCGCAACGCGGACCCCAAACAACUGACACAGCCCGUGAGCUGUACAGG 427

QY 359 AAGCUGAAGAGGAGGAUCACTUCCACGCGCGCCAAAGAGAGUACAGCTUGAGCUACAGCGCC 418
   |||
Db 428 AAGCUGAAGAGGAGGAUCACTUCCACGCGCGCCAAAGAGAGUACAGCTUGAGCUACAGCGCC 487

QY 419 GGCGCCCTUGGCCAGCUGCAUUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGAACACCGAG 478
   |||
Db 488 GGCGCCCTUGGCCAGCUGCAUUGGGCCUGAUCUACAACAGGAUGGGCGCCGUGAACACCGAG 547

QY 479 GUGGCCUUCGGCCUGUGUGGGCCACCTUGCGAGCAGAUUCGCCGACACCGCAGCAGCCGAGC 538
   |||
Db 548 GUGGCCUUCGGCCUGUGUGGGCCACCTUGCGAGCAGAUUCGCCGACACCGCAGCAGCCGAGC 607

QY 539 CACAGGCAGAUUGGACACACCAAACCCCTUGAUCAGGCACGAGAACAGGAUGGUGUGUG 598
   |||
Db 608 CACAGGCAGAUUGGUGAACACCAAACCCCTUGAUCAGGCACGAGAACAGGAUGGUGUGUG 667

QY 599 GCCAGCACCAACCGCAAGGCCAUGGAGCAGAUUGGCCGCGCAGCAGCAGCGCCCGAG 658
   |||
Db 668 GCCAGCACCAACCGCAAGGCCAUGGAGCAGAUUGGCCGCGCAGCAGCAGCGCCCGAG 727

QY 659 GCCAUGGAGUGGCCAGCAGCGCCAGCGCAGAUUGGUGCAGGCCAUGAGGACCAUCGGCACC 718
   |||
Db 728 GCCAUGGAGUGGCCAGCAGCGCCAGCGCAGAUUGGUGCAGGCCAUGAGGACCAUCGGCACC 787

QY 719 CACCCAGCAGACGGCGCGCCUAGAAGACGACCTUGUGGAGAACCTUGCAGGCGCUACCCAG 778
   |||
Db 788 CACCCAGCAGACGGCGCGCGCCUAGAAGACGACCTUGUGGAGAACCTUGCAGGCGCUACCCAG 847

QY 779 AAGCGCAUGGGCGUGCAGAUACGCGGCUUCAAAGUGAAACUAGUGACUGACUAGCCCGCUGG 838
   |||
Db 848 AAGCGCAUGGGCGUGCAGAUACGCGGCGUUAAGUGAACUAGUGACUAGCAGCCCGCUGG 907

QY 839 GCUCUCCAAACGGGCGCUCUCCUCCUGUACCAAAAAAIAAAAAAAAAAAAAAAAAAAAA 898
   |||
Db 908 GCUCUCCAAACGGGCGCUCUCCUCCUCCUGUACCAAAAAAIAAAAAAAAAAAAAAAAAAAAA 967

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Qy 359 AAGCTGAAGAGGAGAUACCUUCCACGGCGCCCAAGGAGAUACCCUGAGCUACAGCGCC 418
Db 383 AAGCTGAAGAGGAGATCACCTTCCACGGCGCCCAAGGAGATCACCTGAGCTACAGCGCC 442
Qy 419 GGGCGCCUUGGCGACGUGCAUGGGGCTUGAUUUAACAACAGGAGUGGCGCGGUGACCAACCGAG 478
Db 443 GGGCGCCCTTGGCAGCTGCATGGGCTGTATCTAACAAGGATGGGCGCGGTGACCAACCGAG 502
Qy 479 GUGGCGUUGGCGUUGUGCGCCACCTUGCGAGCAGAUUGCGCGACAGCCAGCACCGCAGC 538
Db 503 GTGCGCTTGGCGCTGTGCGCCACCTGCGAGCAGATCGCGGACAGCCAGCACCGCAGC 562
Qy 539 CACAGGAGAGUGGAGACACACACAAACCCUUGAGAGGACGACGAGAACAGAGUUGUCUG 598
Db 563 CACAGGAGAGTGGTGACCAACACCAACCCCTGTATCAGGCAAGGACAGAGATGGTGTG 622
Qy 599 GCCAGCACCCCGCCAGAGGCAUGGAGCAGAGUGGCGCGGACGACGAGCGCGCGCGAG 658
Db 623 GCCAGCACCCCGCCAGAGGCAUGGAGCAGATGGCGCGGACGACGAGCGCGCGCGAG 682
Qy 659 GCCAUGGAGUGGCGCAGCAGGCGCAGGAGUGGCGGCAUGAGGACCAUCGCGCAC 718
Db 683 GCCATGAGGTGGCGAGCCAGGCGCAGGAGATGGTGCAGGCGCATGAGGACCATCGGCAC 742
Qy 719 CACCCAGCAGCAGCGCGCGCGUGAAGAACGACUUGGUGGAGAGACCUGCGAGGCGUACAG 778
Db 743 CACCCAGCAGCAGCGCGCGCGTGAAGAACGACCTGTGGAGAACCTGCGAGCGCTACCG 802
Qy 779 AAGCGCAUGGGCGUGGAGAGUACGCGUUAAGUAACUAGU 820
Db 803 AAGCGCATGGGCGTGAGATGACGCGCTTCAANGTGAACACTAGT 844
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RESULT 5
US-10-729-830-5
; Sequence 5, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; PRIOR FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 942
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA with stabilisation sequences
; FEATURE:
; OTHER INFORMATION: The stabilisation sequences are derived from 5' -
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
; OTHER INFORMATION: respectively.
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
; OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-5
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Query Match 70.8%; Score 666.8; DB 8; Length 942;
Best Local Similarity 81.7%; Pred. No. 4.4e-126;
Matches 770; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

Qy 1 GCUUGUUCUUUUGCAGAGCUCAGAAUAAACGCUCAUUGGCGAGAUCAUAAAGUAGAG 60
Db 1 GCUUGUUCUUUUGCAGAGCUCAGAAUAAACGCUCAUUGGCGAGAUCAUAAAGUAGAG 60
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Qy 61 CCUGUGACCGAGGUGGAGACCUUACGUGUGAGCAUCCUCCAGCGGCGCCUUGAAGGC 120
Db 61 UCUUUUUAACCGAGGUGGAGAAACGUAUCGUUCUCUUAUCCCGUCAGGCGCCUCAAAGC 120
Qy 121 CGAGAUUGCGCCAGAGGUGGAGGACGUGUUGCGCGCAAGAACACCGACUGAGGUGUC 180
Db 121 CGAGAUUGCACAGAGACUUGAGAGUGUUGGAGGAGGAGAACACCGAUCUUGAGGUUC 180
Qy 181 GAUGGAGUGGCGUAAAGAACAGGCGCCAUCCUGAGCGCCUUGACCAAGGCAUCCUGGGCU 240
Db 181 CAUGGAUUGGCGUAAAGAACAGGCGCCAUCCUGAGCGCCUUGACCAAGGGAUUTUAGAU 240
Qy 241 CGUUGUACCCUGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db 241 UGUUGUACGCGUCACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Qy 301 CGCGCUGAAACGGGCAACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
Db 301 UGCGCUGAAACGGGCAACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
Qy 361 GCUAAGAGGAGGAUACCUUCCACCGCGCGCAAGGAGAUACGCGGCGGCGGCGGCGG 420
Db 361 GCUCAAAGAGGAGGAUAAACAUUCCUGGCGCGCAAGGAGAUUAAACUGUAAGGAA 420
Qy 421 CGCGCUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
Db 421 UGCAUUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
Qy 481 GCGCUUGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 540
Db 481 GCGAUUUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
Qy 541 CAGGCGAGUUGGUGACCAACCAACCGCGCGCAAGGCGGCGGCGGCGGCGGCGGCGG 600
Db 541 UAGGCGAAUUGGUGACCAACCAACCGCGCGCAAGGCGGCGGCGGCGGCGGCGGCGG 600
Qy 601 CAGCACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
Db 601 CAGCACUACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
Qy 661 CAUGGAGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
Db 661 CAUGGAGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
Qy 721 CCCGAGCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
Db 721 UCCUAGCUCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
Qy 781 GCGCAUGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
Db 781 ACGAAUGGGGGGUGGAGUACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
Qy 841 CUCCCAACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
Db 841 CUCCCAACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
Qy 901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
Db 901 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
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RESULT 6
US-10-729-830-1
; Sequence 1, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
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; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Influenza virus
; FEATURE:
; OTHER INFORMATION: Influenza matrix: wildtype gene (for comparison)
; FEATURE:
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
; OTHER INFORMATION: codon: tga (nucleotides 767 to 769 )
US-10-729-830-1

Query Match      53.0%; Score 498.8; DB 8; Length 774;
Best Local Similarity 65.6%; Pred. No. 6.4e-92;
Matches 508; Conservative 94; Mismatches 172; Indels 0; Gaps 0;

Qy 46 AGAUCUAAAGUAGCCUGUGCGGAGGUGGAGACCUAGGUGGAGCAUCCGUGGAGCAUCCCGAG 105
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 1 AGATCTAAAGATGAGTCTTCTAAACCGAGGTGAAACGCTACGTTCTCTATCATCCCCGTC 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 106 CGGCCCCCUGAAGGCCGAGAUCCGCCAGAGGUGGAGGACGUGUUGCGCCGCAAGAACAC 165
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 AGGCCCTTCAAGCCGAGATGCGACAGAGACTTGAAGATGCTTTTGGAGGGAAGAACAC 120
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 166 CGACUGAGGUGUGAUGGAGUGGUGUGAAGACACGAGGCCCAUCCUGAGCCCCCGACAA 225
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 CGATCTTGAGGTCTCATGTGAATGGCTAAAGACAAGCAATCTGTCACTCTGACTAA 180
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 226 GGGCAUCCUGGCUUGUUAUCCUAGACCCUGACCGGCCAGCGGCGGCGGCGGCGGCGG 285
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 181 GGGGATTTTAGGATTTGTGTTCAACGCTCACCGTCCAGTGGAGGAGGACTGCGAGCGTAG 240
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 286 CGCUUUGUGCAGAACGCCUGAACGGCAACGGGCAACCGGACCCCAACAAUGGACAAGGCCGU 345
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 241 AGCTTTTGTCCAAATGCGCTTATGGGAAACGGGATCCAAATACATGGAACAAGCAGT 300
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 346 GAAGCUGUACAGGAAGCUGAAGAGGAGAUCAUCCUCCAGCGGCCCAAGAGGAUAGAGCU 405
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 301 TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCATGGGCGCAAGAAATCTCACT 360
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 406 GAGCUACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 465
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 361 CAGTTATTTCTGCTGGTGCACTTGCAGTTGTATGGGCGCTCATATACACAGGATGGGGCG 420
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 466 CGUGACACCGAGGUGGCUUUGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 525
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 421 TGTGACCACTGAAGTGGGATTTGGCTGTGTATGTGCAACCTGTGAACAGATTTGCTGATC 480
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 526 CCAGACCGCGACCCACGAGGAGUGGAGACCAACCAACCCCGCGCGCGCGCGCGCGCGGAA 585
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 481 CCAGCATCGGTCTCATAGCAAAATGGTGACAACCAACCAACCACTAATCAGACATGAA 540
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 586 CAGGAGUGUGUGGCGCAGCACCAACCGCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 645
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 541 CAGAATGGTTTTAGCCAGCACTACAGCTTAAGGCTATGGAGCAAAATGGCTGGATCGAGTGA 600
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 646 GCAGGCCCGGAGGCGGAGGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 705
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 601 GUAAGCAGAGAGGCGCATGGAGGTTGCTAGTACGCTAGGCAAAATGGTGCAAGCGATGAG 660
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 706 GACCAUCGGCACCACCGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 765
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 661 AACCAATTGGGACTCATCTAGCTCCAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 766 GCAGGCCUACAGAAAGCCUAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 819
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 721 GCAGGCCCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGAACCTAG 774
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 7
US-10-866-484-9
; Sequence 9, Application US/10866484
; Publication No. US20050013828A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, M.
; APPLICANT: Shneider, A.
; TITLE OF INVENTION: Vaccine Compositions and Methods
; FILE REFERENCE: 25955-003CIP
; CURRENT APPLICATION NUMBER: US/10/866,484
; CURRENT FILING DATE: 2004-06-11
; PRIOR APPLICATION NUMBER: 60/435,500
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 10/741,466
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 986
; TYPE: DNA
; ORGANISM: Influenza A virus
US-10-866-484-9

Query Match      52.8%; Score 497; DB 8; Length 986;
Best Local Similarity 66.5%; Pred. No. 1.6e-91;
Matches 506; Conservative 90; Mismatches 165; Indels 0; Gaps 0;

Qy 56 AUGAGCCUGUGAGCCGAGGUGGAGACCUAGGUGGAGCAUCCCGAGGCGGCGGCGGCGG 115
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 1 ATGAGTCTTCTAACCGAGGTGCAAAACGTACGTTCTCTATCGTCCGTCAGGCGGCGGTC 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 116 AAGCCCGAGAUCCCGCAGAGGCGUGGAGCGUGUUGCGCGCAAGAACACCGACCUAGG 175
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 AAGCCGAGATCGGCGAGAGACTTGAAGATGTCTTGTGGGAAGAACCCGATCTCGAG 120
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 176 GUGCUGAUGGAGGUGGUGAAGACAGGCGCCCAUCCUGAGCGGCGGCGGCGGCGGCGG 235
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 GCATCTATGAATGGCTAAAGACAAGACCAATCTGTCTGCTGACTTAAGGGGATTTTA 180
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 236 GGUUUGUGUUAUCCUGAGCCGUGCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 295
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 181 GGAATTTGTGTCAGCTCACCGTCCCGTGCAGTGAGCGAGGAGCTGCGAGCGGTAGACG 240
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 296 CAGAACCCCGCAGAACCGGCGCCCAACCAACAAUGGACAGGCGGCGGCGGCGGCGGCGG 355
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 241 CAGAAATGCCCTTATGGGAATGGGGATCCAAACAAACATGGACAGGCGAGTGAACCTG 300
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 356 AGGAAGCUGAAGAGGAGAUCAUCCUCCAGGCGCCCAAGGAGAUCAAGCGGAGCUACAGC 415
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 301 AGGAAGCTCAAGAGGAAATTAATTCATCCAGGGGCGCAAGAGTAGCGCTCAGTTATTCT 360
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 416 GCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 475
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 361 ACTGGTGCATTTGCGAGCTGCATGGGCTCATATACACAGAAATGGGAGCTGTAAACCACT 420
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 476 GAGGUGGCGCUUCCGCGGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 535
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 421 GAAGTGGCAATTTGGCCCTAGTGTGTGGCCATTTGTGAGCAGATTTGCCGACTCCAGCATCG 480
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 536 AGCCACAGGCGAGUUGGAGCAACCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 595
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 481 TCCACACAGACAGATGGTGACGACAAACCAACCCACTAATCAGACATGAGACAGGATGGTG 540
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 596 CUGGCGCAGCACCGGCAAGGGCGCAUGGAGGAGUUGGCGGCGGCGGCGGCGGCGGCGGCGG 655
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 541 CTGCGCAGTACCAACCGCTAAGGGCCATGGAGCAGATGGCAGGCTCGAGTGAACAGGCGAGCA 600
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 656 GAGGCCAUGGAGGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 715
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 601 GAAGCCATGAGGTTGTAGTTCAGGCTAGGCGAGATGGTGCGGCAATGAGAAACCATTTGGG 660
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 716 ACCCAACCCAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 775
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 661 ACTCACCTAGCTCAGTCCGGTCTAAAGATGATCTCTTGAAATTTGCAGGCCTAC 720
Qy 776 CAGAAGCGCAUGGCGUGCAGUAGCAGCGCUUCAAGUAC 816
Db 721 CAGAAACGGATGGAGTGCAATGACGAGTTCAGTGATC 761

RESULT 8

US-10-177-390-31
; Sequence 31, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Influenza virus
US-10-177-390-31

Query Match 52.0%; Score 489.4; DB 6; Length 1027;
Best Local Similarity 65.2%; Pred. No. 5.6e-90;
Matches 503; Conservative 92; Mismatches 176; Indels 0; Gaps 0;
Qy 46 AGAUCUAAAGUAGCCUGCUGACCGAGGUGAGACCUACUGUGUGAGCAUCAUCCCCAG 105
Db 16 ATATTGAAAGATGAGTCTTAAACCGAGGTGAAACGTACGTTCTCTATCATCCCGTC 75
Qy 106 CGGCCCCUGAAGCGCGAGUAGCCCGCAGGCGUGAGACGUGUUCGCGCGCAGAACAC 165
Db 76 AGGCCCCCTCAAGCCGAGATCGCACAGAGACTTGAAGATGCTTTGCGAGGGAAGAACAC 135
Qy 166 CGACUUGAGUGUGUGAGUGGUGAAGACAGGCGCCCAUCCUGAGCCCCUGACCA 225
Db 136 CGATCTTGAGGTTCTCATGGAATGGCTAAAGACAGACCAATCTGTCACTCTGACTNA 195
Qy 226 GGGCAUCCUGGCUUUGUUGUACCCUGACCGGCCAGCGCGCCUGCAGCGCGCG 285
Db 196 GGGGATTTTAGGATTTGTGTTCAAGCTCAGCGTCCCGTCCAGTGAAGGACTGCGACGTAG 255
Qy 286 CCGCUUCUGCAGACCGCCUGAAGCGCAACGGGACCCCAACACAGUAGGACAGGCGGU 345
Db 256 ACGCTTTGTCCAAATGCCCTTAAATGGGAACGGGGATCCAAATACATGGHCAAGCAGT 315
Qy 346 GAAGCUGUACAGGAAGCUGAAGGAGAGAUCAUCCUACCGCGCGCAAGGAGAUACAGCU 405
Db 316 TAAACTGTATAGGAAGCTCAGAGGGAGATACATTCATGGGCGCAAGAAATCTCACT 375
Qy 406 GAGCUACAGCCGCGCGCCUGGCGCAGCUGAUGGGCCUGAUUACACAGAUUGGGCGC 465
Db 376 CAGTTATTCTGCTGTCAGCTTGCAGTTGTATGGGCTCATATACACAGGATTTGTGACTC 435
Qy 466 CGUACACCGAGUGGCGCUUGGCGGUGGCGCCACCUCCGAGCAGAUUGCGGCGCAG 525
Db 436 TGTGACCACTGAAGTGGATTTGGCGCTGTATGTGCAACCTGTGAAACAGATTTGTGACTC 495
Qy 526 CCAGCAGCGCACAGGAGUUGUACACCAACCAACCCUUGAUGAGCGACGAGAA 585
Db 496 CCAGCATCGGTCTCATAGGCAATGGTGACACACACCAACCACTAATCAGACATGAGAA 555
Qy 586 CAGAUUGUGUGGCGCAGCACACCGCCAAAGCCCAUGAGCAGAUUGGCGCGAGCAGGA 645
Db 556 CAGAAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAAATGGCTGATCGAGTGA 615
Qy 646 GCAGGCCCGCGAGGCGCAUGGAGGCGCCAGCCAGGCGCAGGCGAGUUGGCGGCGCAUGAG 705

Db 616 GCAGCAGCAGAGGCCATGGAGTTGCTAGTCAGGCTAGGCAATGGTCAAGCGATGAG 675
Qy 706 GACCAUCGGCACCCACCCAGCAGCAGCGCGCGCCUGAAGAACGACCUUGUGAGAACCU 765
Db 676 AACCAITGGGACTCATCTAGCTCCAGTGTGCTGTGAAAAATGATCTTTTGAATAATTT 735
Qy 766 GCAGGCGUACCAAGCGGCAUGGCGCGCUGCAGUAGCAGCGCUUCAAGUAGAC 816
Db 736 GCAGGCGCTATCAGAAACGAATGGGGTGCAGATGCAACGGTTTCAAGTGATC 786

RESULT 9

US-10-855-875-5
; Sequence 5, Application US/10855875
; Publication No. US20050003349A1
; GENERAL INFORMATION:
; APPLICANT: Kawaoaka, Yoshihiro
; TITLE OF INVENTION: High Titer Recombinant Influenza Viruses for Vaccines and Gene T
; FILE REFERENCE: 800.038US1
; CURRENT APPLICATION NUMBER: US/10/855,875
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: US 60/473,798
; PRIOR FILING DATE: 2003-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Influenza virus
US-10-855-875-5

Query Match 51.8%; Score 487.8; DB 8; Length 1027;
Best Local Similarity 64.6%; Pred. No. 1.2e-89;
Matches 503; Conservative 94; Mismatches 182; Indels 0; Gaps 0;
Qy 46 AGAUCUAAAGUAGCCUGCUGACCGAGGUGAGACCUACUGUGUGAGCAUCAUCCCCAG 105
Db 16 ATATTGAAAGATGAGTCTTAAACCGAGGTGCAACGATGCTCTCTATCATCCCGTC 75
Qy 106 CGGCCCCUGAAGCGCGAGAUCCGCCAGGCGUGGAGGACGUGUUCGCGCGCAGAACAC 165
Db 76 AGGCCCCCTCAAGCCGAGATCGCACAGAGACTTGAAGATGCTTTTGCAGGGAAGAACAC 135
Qy 166 CGACUUGAGGUGUGAUGGUGUGAAGACAGGCGCCCAUCCUGAGCCCCUGACCA 225
Db 136 CGATCTTGAGGTTCTCATGGAATGGCTTAAAGACAGACCAATCTGTCTCTGACTAA 195
Qy 226 GGGCAUCCUGGCGCUUCUGUUGUACCCUGACCGCGCGCGCGCGCGCGCGCGCGCG 285
Db 196 GGGGATTTTAGGATTTGTGTTCAAGCTCAGCGTCCCGTCCAGTGAAGGACTGCGACGTAG 255
Qy 286 CCGCUUCUGCAGAACCGCCUGAAGCGGCAACGGGACCCCAACAAUGACAAAGGCGGU 345
Db 256 ACGCTTTGTCCAAATGCCCTTAAATGGGAACGGGATCCAAATACATGGCAAAAGCAGT 315
Qy 346 GAAGCUGUACAGGAAGCUGAAGGAGAGAUCAUCCUACCGCGCGCGCGCGCGCGCGCG 405
Db 316 TAAACTGTATAGGAAGCTCAGAGGGAGATAACATTCATGGGCGCGCGCGCGCGCGCG 375
Qy 406 GAGCUACAGCG 465
Db 376 CAGTTATTCTGCTGTCAGCTTGCAGTTGTATGGGCTCATATACACAGGATTTGTGACTC 435
Qy 466 CGUACACCGAGUGGCGCUUCGCGCGUGGUGGCGCCACCUCCGAGCAGAUUGCGGCGCAG 525
Db 436 TGTGACCACTGAAGTGGCAATTTGGCGCTGTATGTGCAACCTGTGTGAACAGATTTGTGACTC 495
Qy 526 CCAGCAGCGCACAGGAGUUGUACACCAACCAACCCUUGAUGAGCGACGAGAA 585
Db 496 CCAGCATCGGTCTCATAGGCAATGGTGACACACCAACCACTAATCAGACATGAGAA 555
Qy 586 CAGAUUGUGUGGCGCAGCACACCGCCAAAGCCCAUGAGCAGAUUGGCGCGAGCAGGA 645
Db 556 CAGAAATGGTTTTAGCCAGCACTACAGCTAAGGCTATGGAGCAAAATGGCTGATCGAGTGA 615
Qy 586 CAGGAGGUGUGGCG 645

Db 556 CAGAAATGGTTTATGACGAGCTTACAGCTTAAGGCTATGGAGCAAAATGGCTGGATCGAGTGA 615
Qy 646 GCAGGCGCCGAGGCGCAUGGAGGUGGCCAGGCGAGGCGAGGUGGUGGCGGCGCAUGAG 705
Db 616 GCAGCAGAGGAGGCGCATGGAGGTTGCTAGTCAGCTAGACAAATGGTGCAAGCGATGAG 675
Qy 706 GACCAUCCGACCCACCCAGCAGCAGCGCGCGGCGUGAAGAACGACCCUGGAGAACCU 765
Db 676 AACCAATGGGACTCATCTAGCTCCAGTGCTGGTCTGAAATAATGATCTCTTGAAATTT 735
Qy 766 GCAGGCUACAGAGCGCAUGGCGUGGCGUGGCGUGGCGUGGCGUGGCGUGGCGUGGCG 824
Db 736 GCAGGCGCTATCAGAAACGAATGGGGGTGCAGATGCAACGGTTCAAGTGTATCTCTCACT 794

RESULT 10

US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE: misc feature
; NAME/KEY: (673)..(673)
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-065-133A-1

Query Match 51.7%; Score 487.4; DB 6; Length 1023;
Best Local Similarity 65.0%; Pred. No. 1.4e-89;
Matches 501; Conservative 93; Mismatches 177; Indels 0; Gaps 0;
Qy 46 AGAUCUAAAGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 105
Db 15 ATATTTAAAGATGAGTCTCTGACCGAGGTGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 74
Qy 106 CGGCGCCGCGGAGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 165
Db 75 AGGCGCCCTCAAGCGGAGATCGCGCAGAGACTTGAAGATGCTTTGCGGGAAGAACAC 134
Qy 166 CGACGUGAGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 225
Db 135 CGATCTTGAGGCACTCATGTAATGGCTAAAGACAGACCAATCTGTCACTCTGACTAA 194
Qy 226 GGGCAUCCUGGCGTUGGUGUACCCUGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 285
Db 195 AGGGATTTTAGGATTCGTATTCAGCTCACCGTGCCTGCGGCGGCGGCGGCGGCGGCGGCG 254
Qy 286 CGGCUUCGCGAGACCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 345
Db 255 ACGCTTTTGCCAAATGCCCTTAGTGGAAACGGAGATCCAAACCAACATGGGACAGAGCAGT 314
Qy 346 GAAGCUGUACAGGAAGCUGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 405

Db 315 AAAAATGTAAGGAGGCTTAAAGAGAAATAACATTCATCGGCGGCAAAAGAGGTGGCACT 374
Qy 406 GAGCUACAGCG 465
Db 375 CAGCTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
Qy 466 CGUACACCGAGGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 525
Db 435 TGTGACAAACGAAAGTGGCAATTTGGCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494
Qy 526 CCAGCAGCG 585
Db 495 CCAGCATCGATCTCTACAGGCGAGATGGTGACAAACCAACCAACCAATTAATCAGACATGA 554
Qy 586 CAGGAUGGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 645
Db 555 CAGAAATGGTATTTAGCCAGTACCAGGCTAAAGCCATGGAGCAGATGGCAGGCGGTGAGTGA 614
Qy 646 GCAGGCG 705
Db 615 GCAGCAGCAGAGGCGCATGGAGGTTGCTAGTAAGCTAGGCGAGATGCTRCAGGCAATGAG 674
Qy 706 GACCAUCCGACCCACCCAGCAGCAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 765
Db 675 AACCAATGGGAGCCACCCCTAGCTCCAGTCCCGGTTTGAAGATGATCTCTCTTGAATAAT 734
Qy 766 GCAGGCGUACAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 816
Db 735 GCAGGCGCTACCAAGAAACGGATGGGAGTGCAGGATTCAGGATTC 785

RESULT 11

US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE: misc feature
; NAME/KEY: (663)..(663)
; LOCATION: (663)..(663)
; OTHER INFORMATION: At nucleotide 663, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-434-811A-1

Query Match 51.7%; Score 487.4; DB 7; Length 1023;
Best Local Similarity 65.0%; Pred. No. 1.4e-89;
Matches 501; Conservative 93; Mismatches 177; Indels 0; Gaps 0;
Qy 46 AGAUCUAAAGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 105
Db 15 ATATTTAAAGATGAGTCTCTGACCGAGGTGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 74


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Db 495 CCAGCATCGATCTCACAGGACAGATGGTGACATTAACCAACCCATTAATCAGACATGAAGA 554
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Qy 706 GACCAUCGCGACCCACCCAGCAGCAGCGCGCGGCGUGAAGAACGACCGUGGAGAGAACCU 765
Db 675 AACCATTTGGGACCCACCCCTAGCTCCAGTGCGGGTTGAAAGATGATCTCCTTGAATAATT 734
Qy 766 GCAGGCGUACAGAAAGCGCAUGGCGUGCAGAUAGCAGCGCUUCAAGUGAAC 816
Db 735 GCAGGCGCTACCAGAAACGGATGGGAGTGCAAAATGCAGCGATTCAAGTGATC 785

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; Sequence 4, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EO-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
US-10-434-811A-4

Query Match 51.4%; Score 484.6; DB 7; Length 1023;
Best Local Similarity 64.9%; Pred. NO. 5.3e-89;
Matches 500; Conservative 92; Mismatches 179; Indels 0; Gaps 0;

Qy 46 AGAUCAAAGAUGAGCGCUGAGCGAGGUGGAGACCUACGUGUGAGCAUCCGCCAG 105
Db 15 ATATTTAAAGATGATGCTTCTGACCGAGGTGGAACGTACGTTCTCTCTATCTTACCATC 74
Qy 106 CGGCCCCCUGAAGCGCGAGUUCGCCAGAGGCGAGGAGCGUGUUCGCCGCAAGAACAC 165
Db 75 AGGCCCCCTCAAAGCGGAGATCGCGCAGAGACTTGAAGATGCTTTTGGCAGGGAAGAACAC 134
Qy 166 CGACUGAGGUGUGUGAGGAGGUGCUAAGACCCAGGCGCCCAUCCUGAGCCCCUGACCAA 225
Db 135 CGATCTTGGAGGCATCTATGGAATGGCTAAAGACAAGACCAATCCTGTGTCTGACTGATA 194
Qy 226 GGGCAUCCUGGCGUUCUGUUCACCCUGAGCGAGCGCGCGCGCCUGCAGCGCGCG 285
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Qy 406 GAGCUCACAGCGCGCGCGCCCGGCGCAGCAGCAGUUGGCGCUUAGUACAAACAGGAUGGCGCG 465
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Db 435 TGTGACAAACCGAAGTGGCATTTGGCCTGGTATGCGCCACATGTGAACAGATCGCTGATTC 494
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Db 495 CCAGCATCGATCTCAACAGGACAGATGGTGACAATAACCAACCCATTAATCAGACATGAAGA 554
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Db 555 CAGAATGGTATTAGCCAGTACCAACGCGCTAAAGCCATGGAGCAGATGCGCGGTGAGTGA 614
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Db 615 GCAGGCGAGCAGAGGCCATGGAGGTGTCTAGTAAGGCTAGGCGAGATGGTACAGGCAATGAG 674
Qy 706 GACCAUCGCGCACCCACCCAGCAGCAGCGCGCGCGCUGAAGAACGACCGUGGAGAGAACCU 765
Db 675 AACCATTTGGGACCCACCCCTAGCTCCAGTGCGGGTTTGAAGATGATCTCCTTGAATAATT 734
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Job time : 927.936 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2006, 23:50:55 ; Search time 428.115 Seconds
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Perfect score: 942
Sequence: 1 GCUCUCUCUCUUUUUCGACAG.....aaaaaaaaaaaaaaaa 942

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Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0

UNITED STATES DEPARTMENT OF JUSTICE

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq.*
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4: /cgn2_6/ptodata/2/pubpna/PCT NEW PUB.seq.*
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13: /cgn2_6/ptodata/2/pubpna/US60 NEW PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	733.6	77.9	756	12	US-11-131-479-27	Sequence 27, Appl
2	692.8	73.5	1050	12	US-11-131-479-59	Sequence 59, Appl
3	688.6	73.1	759	12	US-11-131-479-69	Sequence 69, Appl
4	668.4	71.0	982	12	US-11-131-479-61	Sequence 61, Appl
5	667.8	70.9	759	12	US-11-131-479-79	Sequence 79, Appl
6	597.6	63.4	756	12	US-11-131-479-28	Sequence 28, Appl
7	491	52.1	756	12	US-11-131-479-26	Sequence 26, Appl
8	484.6	51.4	1027	12	US-11-131-479-3	Sequence 3, Appl
9	476	50.5	1305	12	US-11-131-479-45	Sequence 45, Appl
10	463.4	49.2	987	12	US-11-155-478A-131	Sequence 131, Appl
11	457.6	48.6	4822	12	US-11-131-479-95	Sequence 95, Appl
12	457.6	48.6	7798	12	US-11-131-479-97	Sequence 97, Appl
13	457.6	48.6	7798	12	US-11-131-479-98	Sequence 98, Appl
14	457	48.5	982	12	US-11-131-479-60	Sequence 60, Appl
15	457	48.5	5161	12	US-11-131-479-101	Sequence 101, Appl
16	457	48.5	5398	12	US-11-131-479-91	Sequence 91, Appl
17	457	48.5	7798	12	US-11-131-479-99	Sequence 99, Appl
18	457	48.5	7798	12	US-11-131-479-100	Sequence 100, Appl
19	457	48.5	8442	12	US-11-131-479-106	Sequence 106, Appl
20	457	48.5	8442	12	US-11-131-479-107	Sequence 107, Appl

21	457	48.5	8450	12	US-11-131-479-104	Sequence 104, Appl
22	457	48.5	8450	12	US-11-131-479-105	Sequence 105, Appl
23	455.8	48.4	1027	12	US-11-155-478A-130	Sequence 130, Appl
24	401.8	42.7	629	9	US-11-137-807-18	Sequence 18, Appl
25	77.4	8.2	1180	12	US-11-116-746-2	Sequence 2, Appl
26	77.4	8.2	1180	12	US-11-116-746-4	Sequence 4, Appl
27	75.8	8.0	588	12	US-11-136-527-1488	Sequence 1488, Appl
28	75.8	8.0	588	12	US-11-136-527-5584	Sequence 5584, Appl
29	75.4	8.0	1677	7	US-10-515-547-3	Sequence 3, Appl
30	75.2	8.0	4339	8	US-10-509-125-801	Sequence 801, Appl
31	74.8	7.9	2475	9	US-11-197-133A-17	Sequence 17, Appl
32	74.8	7.9	5152	8	US-10-240-708-47	Sequence 47, Appl
33	74.6	7.9	1395	8	US-10-955-058A-111	Sequence 111, Appl
34	74.6	7.9	2217	8	US-10-947-249-197	Sequence 197, Appl
35	74.6	7.9	3819	7	US-10-973-115B-405	Sequence 405, Appl
36	74.6	7.9	3819	8	US-10-131-826A-405	Sequence 405, Appl
37	74.4	7.9	600	12	US-11-136-527-6371	Sequence 6371, Appl
38	74.4	7.9	2020	12	US-11-090-617-697	Sequence 697, Appl
39	74.9	30.15	12	US-11-183-136-39	Sequence 39, Appl	
40	74.4	7.9	4409	12	US-11-136-527-2275	Sequence 2275, Appl
41	74.2	7.9	1905	8	US-10-947-249-132	Sequence 132, Appl
42	74	7.9	1690	12	US-11-090-439-43	Sequence 43, Appl
43	73.8	7.8	588	8	US-10-689-742-41	Sequence 41, Appl
44	73.6	7.8	762	9	US-11-096-568A-12243	Sequence 12243, A
45	73.5	7.8	2566	12	US-11-091-883-36	Sequence 36, Appl

ALIGNMENTS

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RESULT 1
US-11-131-479-27
; Sequence 27, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein
US-11-131-479-27

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	Query Match	77.9%;	Score 733.6;	DB 12;	Length 756;
	Best Local Similarity	86.2%;	Pred. No. 2.2e-77;		
	Matches 652;	Conservative	90;	Mismatches 14;	Indels 0; Gaps 0
Qy	56	AUGAGCCUGUGACCGAGGUGGAGACCUACGUGCUGAGCAUCAUCCACGAGGCCCCCUG	115		
Db	1	ATGAGCCTGCTGACCGAGGTGGAGACCTAGCTGCTGAGCATCTATCCACAGGCCCCCTG	60		
Qy	116	AAGGCCGAGAUCCGCCAGAGCGUGGAGGACGUGUUCGCGCGCAAGAACACCCAGACUGGAG	175		
Db	61	AAGGCCGAGATCGCCAGAGGCTGGAGGACGTGTTCCGCGCGAGAAACACCGACCTGGAG	120		
Qy	176	GUGCUGAUGGAGUGGCGUGAAGACACAGGCCCAUCCUGAGCCCCCUUGACCAAGGGCAUCCUG	235		
Db	121	GTGCTGATGAGTGGCTGAAGACACAGGCCCATCTCTGAGCCCCCTGACCAAGGGCATCTTG	180		

Db 421 GAGGTAGCCTTTGGCCTTGGTCTGCGCCACTTGGCAGCAGATCGCGCACTCTCAGCATAGA 480
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Db 481 TCTCACAGACAGATGGTGACGACTACAAACCCCTTGATACGCGCAGAACAGGATGGT 540
Qy 596 CUGGCCAGCACCCCGCCAAAGCCCAUGGAGCAGAUUGGCCGCGCAGCAGCGCCGCC 655
Db 541 CTGGCCTCTACTACCGCCCAAGCCCATGGAGCAGATGGCGCGCAGCAGTGAGCAGCGCC 600
Qy 656 GAGGCAUGGAGUGGCGCAGCCAGCCAGCGCAGCAGAUUGGUGCAGGCAACCAUUGGC 715
Db 601 GAGGCGATGGAGGTAGCTCTCAGGCCAGGCGAGATGGTGCAGGCCATCGGAACCATCGGC 660
Qy 716 ACCCAACCCAGCAGCAGCGCGCCUUGAAGAACGACCUUGUGGAGAACCUUGCAGGCCUAC 775
Db 661 ACTCACCCCTCAGCTCTGCGGCCCTGAAGAACGACCTGCTTGGAAACCTCGAGGCCCTAT 720
Qy 776 CAGAACGCGAUGGCGUGCAGAUAGCAGCGCUUCAAAG 811
Db 721 CAGAACGAGAAATGGCGGTACAGATGCAGAGGTTTCAAG 756

RESULT 7
US-11-131-479-26
; Sequence 26, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein
US-11-131-479-26

Query Match 52.1%; Score 491; DB 12; Length 756;
Best Local Similarity 66.2%; Pred. No. 3e-49;
Matches 500; Conservative 90; Mismatches 165; Indels 0; Gaps 0;
Qy 56 AUGACCGUGUACCGAGGUGGAGACCUAGCUGUGCGCAUCAUCCCGAGCGCCCGCCUG 115
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Qy 116 AAGCCGAGAUCCGCCAGAGGUGGAGCAGCUGUUGCCGCGCAAGAACACCGACUGAG 175
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Qy 176 GUGCUGAGGAGUGGCUAGAACCGCCAGCCAUCCUGGAGCCCGCCUGACCAAGGGCAUUCUG 235
Db 121 GTATTGATGGATGGCTGAAACCGGACCTATTCTGAGCGCCCTGACTAAGGGAACTACTC 180
Qy 236 GGUUCUGUUGUACCCUAGCCGUGCCAGCGAGCGCGCCUGCAGCGCGCGCCUGUCUG 295
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Qy 296 CAGAACCGCCUAGAACCGGCAACCGGACCCCAACAAUAUGGACAAAGGCCUGAAGCUGUAC 355
Db 241 CAGAACGCTTTAAACGGGAAACGGGACCCCAATAATATGGATTAAGGCAGTGAACCTGTAT 300

Qy 356 AGAAGCUGAAGAGGAGAUCAUCCUACCGGCGCCAAAGGAGAUCAUAGCCUGAGCUACAGC 415
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Qy 416 GCGGCGCCUUGGCGCAGCUGCAUGGCGCUUGAUUAACAGGAUGGCGCGCGUGACCAACC 475
Db 361 GCAGGTCTCTCGCGTCTGTATGGGACTTATCTACAACCGAATGGGCGCGTCAACAACA 420
Qy 476 GAGGUGGCCUUCGCGUGGUGCGCCACCUUGCGGAGCAGAUUGCCGAGCAGCAGCACCGC 535
Db 421 GAAGTGGCTTTTCGGGCTGGGTGGCAACTTTCGCAACAGATTGCTGACAGTCAGACCCGG 480
Qy 536 AGCCACAGGCGAGAUUGGUGACCAACCAACCCUUGAUCAGGCGACGAGAACAGGAUGUG 595
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Qy 656 GAGGCCAUGGAGUGGCGCAGCGCCAGCAGCAGAUUGGCGCAUAGAGGACCAUCCGCGC 715
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Qy 716 ACCCAACCCAGCAGCAGCGCGCCUGAAGAACGACCUUGUGGAGAACCUUGCAGGCCUAC 775
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Db 721 CAAAAGCGGATGGGCGTCCAGATGCAGAGATTTAA 755

RESULT 8
US-11-131-479-3
; Sequence 3, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Influenza A virus
US-11-131-479-3

Query Match 51.4%; Score 484.6; DB 12; Length 1027;
Best Local Similarity 64.9%; Pred. No. 1.6e-48;
Matches 500; Conservative 92; Mismatches 179; Indels 0; Gaps 0;
Qy 46 AGAUCUAAAGAUAGCCUGCUGACCGAGGUGGAGACCUAGCUGUGAGCAUCAUCCCCAG 105
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Qy 526 CCAGCACCGCAGCACAGGAGUGGAGUACCAACCAACCCCGUAGUACAGCGACGAGAA 585
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RESULT 9
US-11-131-479-45
; Sequence 45, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 1305
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Influenza A Virus M1 Fused to Synthetic HBcAg
US-11-131-479-45

Query Match 50.5%; Score 476; DB 12; Length 1305;
Best Local Similarity 64.9%; Pred. No. 1.5e-47;
Matches 491; Conservative 90; Mismatches 175; Indels 0; Gaps 0;

Qy 56 AUGAGCUCUGACCCAGGUGGAGACCUAGUCUGAGCAUACUCCCGAGCGGCCCCUG 115
Db 1 ATGAGTCTTCTAACCCGAGGTGAAACGTACGTACTCTTATCATCTCCGTAGGCGCCCTC 60
Qy 116 AAGGCCAGAUCCGCCAGAGGCGUGGAGCGUGUCCGCCGGAAGAACACACCGACCCUGGAG 175
Db 61 AAAGCCGAGATCGCANAGACTTTGAAGATGTCTTTGCAGGGAAGAACACTGATCTTGAG 120
Qy 176 GUGCUGAUGAGUGGUGGAAAGACAGGCCCAUCUGAGCCCCCUGACCAAGGGGCAUCCUG 235
Db 121 GTTCTCATGAATGGCTTAAAGACAAGACCAATCTGTCACTCTCTAAGGGGATTTTA 180
Qy 236 GGCUCUGUUCUACCCUGACCGUGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 295
Db 181 GGAATTTGTGTCACTGCGTCACTGCGGCGGAGGAGGACTGCGAGCGTAGACGCTTTGTG 240
Qy 296 CAGAACCCCCUGAACCGCAACGGCGACCCCAACAUAUGGACAAGGCCGCGUGAAGCUGUAC 355
Db 241 CAAATGCCCTTAAATGGGAACGGGGATCCAAATTAACATGACAAAGCAGTTAACTGTAT 300
Qy 356 AGGAAGCUGAAGAGGGAGAUACCUUCCAGCGGCCCAAGGAGAUACGCCUGAGCUACAGC 415
Db 301 AGGAAGCTCAAGAGGGAGATAACATTCATGGGGCCAAAGAAATCTCACTCAGTTATCT 360
Qy 416 GCGGCGCCCGGCGCAGCUCUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 475
Db 361 GCTGGTGCACTTGGCCAGTTGTATGGGCTCATATACAAAGGATGGGGGCTGTGACCACT 420
Qy 476 GAGUGGCGCUUCCGCGUGUGUGCGCCAGCGAGCAGAUCCGCCAGCGGCGGCGGCGGCGG 535
Db 421 GAAGTGGCATTTGGCCTGGTATGTGCACTGTGAAACAGATTGCTGACTCCAGCATCGG 480
Qy 536 AGCCACAGGAGUGGUGACCAACCAACCCCGCUGAUGAGGCAAGGAGAAACAGAUUGUG 595
Db 481 TCTCATAGGCAATGGTGACAAACCAATCCACTAATCAGATGAGAAACAGAAATGGTT 540
Qy 596 CUGGCGCAGCACCCCGCAAGGCCCAUGGAGCAGAUCCGCCAGCGGCGGCGGCGGCGGCGG 655
Db 541 TTAGCCAGCACTACAGCTAAGGGTATGGAGCAATGGCTGGATCGAGTGAGCAAGCAGCA 600
Qy 656 GAGGCCAUGAGGUGGCGCAGCGCAGGCGCAGAGUGGUGGAGGCGCAUGAGGACCAUCGCG 715
Db 601 GAGCCATGGAGGTTGCTAGTCAAGCTAGACAAATGGTGCAGCGATGAGAACCATTTGGG 660
Qy 716 ACCCACCCAGCAGCAGCGCGCGGCGGAGAAACGACCUUGCUGGAGAAACCUUGCAGGCCUAC 775
Db 661 ACTCATCTAGTCCAGTGGTCTGAAAAATGATCTTCTGAAAAATTTTGCAGGCGCTAT 720
Qy 776 CAGNAGCGCAUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 811
Db 721 CAGAAACGAATGGGGGTGCAGATGCAACGCGTTCAAG 756

RESULT 10
US-11-155-478A-131
; Sequence 131, Application US/11155478A
; Publication No. US2006001410A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE LAVAL
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 174

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 987
; TYPE: DNA
; ORGANISM: human Influenza A virus
; FEATURE:
; NAME/KEY: Gene
; LOCATION: (1)...(987)
; OTHER INFORMATION: human Influenza A virus
; OTHER INFORMATION: strain A/Charlottesville/31/95 (H1N1)
; OTHER INFORMATION: accession number af398876
US-11-155-478A-131

Query Match      49.2%; Score 463.4; DB 12; Length 987;
Best Local Similarity 63.9%; Pred. No. 4.6e-46;
Matches 486; Conservative 89; Mismatches 186; Indels 0; Gaps 0;

Qy 56 AUGAGCCUGUGACCGAGGUGAGACCUAGUGUGAGUAUCCCGAGCGGCCCGUG 115
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 ATGAGTCTTAAACCGAGGTGAAACGTACGTCTCTCTATCGTCCCGTCAGGCGCCCTC 60

Qy 116 AAGCCGAGUGCCCGACAGCGUGAGACGUGUUGCGCGGCAAGACACCGACUGAG 175
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 AAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTGTGGAAGAAGACACCGATCTTGAG 120

Qy 176 GUGUGAGUGAGUGGUGAAACACAGCGCCCAUCCUGAGCCCGCCUGACCAAGGCAUCCUG 235
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 GCTCTCATGGAGTGGCTAAAGACAAGACCGATCTCTGTACCTCTGACTAAGGGGATTTTA 180

Qy 236 GGUUUGUGUACCCUGACCGUGCCAGCGAGCGCGCCUGCAGCGCCCGCGUUGUG 295
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
181 GGAATGTGTTCACGCTCACCGTGCAGTGCAGGAGGACTGCAGCGTAGACGCTTTGTC 240

Qy 296 CAGAACGCCUGNACGGCAACGGCGACCCCAACACUAGUACAGGCGCGUAGCUAC 355
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
241 CAAATGCCCTTAATGGGAATGGGGATCCAAATAACATGAGCAGAGCATTAATCTGTAT 300

Qy 356 AGGAAGCUGAAGAGGAGUAUACCUUCCACCGCGCAAGGAGAUACGCGCUGAGCUACAGC 415
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
301 AGAAGCTTAAGAGGAGATTAACATTCATGGGCGCAAGAATAAGCACTCAGTTATCT 360

Qy 416 GCGGCGCCCGUGGCGAGCUGCAUGGGCCUGAUUUAACAAGAGUGGGCGCGUGACCAAC 475
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
361 GCTGTGCACCTTGCCAGTTGTATGGGCTCATATACACAGGATGGGGCTGTGACCACC 420

Qy 476 GAGUGGCGCUUGCGCGUGUGCGCCACUGCGAGGAGAUUGCGGACAGCAGCGCC 535
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
421 GAATCAGCATTTGGCCCTGATATGCGCAACCTGTGAACAGATTTGTGACTCCAGCATTAAG 480

Qy 536 AGCCACAGCGAGUGGUGACCAACCAACCCUUGAUCAGGCGACGAGAACAGGAGUGUG 595
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
481 TCTCATAGCAAAATGGTAAACAACCAACCAATCAATTAAGACATAGAACAGATGGTT 540

Qy 596 CUGGCGACACACCGCCAGGCGCAUGGAGCAGAUUGGCGGCGAGCAGCGAGCGCGCC 655
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
541 CTGGCCAGCACTACAGCTAAAGCTATGAGCAAAATGGCTGGATCGAGTGAACAAGCAGCT 600

Qy 656 GAGGCAUGGAGGUGGCGAGCGCCAGGCGAGGAGUUGGCGAGGCAUAGAGACCAUUGCG 715
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
601 GAGGCGATGGAGGTTGCTAGTCAGGCGAGGCAAAATGGTGCAGGCAATGAGAGCCATTGGG 660

Qy 716 ACCACCCAGCAGCGCGCGCCUGAAGAACCAACACCUUGUGGAGAACUUGCAGCGCUAC 775
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
661 ACTCATCTAGCTTAGCACTGGTCTGAANAATGATCTTCTTGAANAATTCAGGCGCTAT 720

Qy 776 CAGAGCGCAUGGGCGUGCAGAUAGCAGCGCUUCAAGUAAC 816
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721 CAGAAACCAATGGGGTGCAGATGCAACGATTCAAGTGATC 761

RESULT 11
US-11-131-479-95
; Sequence 95, Application US/11131479
```

```
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95
; LENGTH: 4822
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4764, Ligation of VR4756 RV-Sali into VR10682 RV
US-11-131-479-95

Query Match      48.6%; Score 457.6; DB 12; Length 4822;
Best Local Similarity 62.1%; Pred. No. 1.6e-45;
Matches 487; Conservative 93; Mismatches 204; Indels 0; Gaps 0;

Qy 33 GCUCACUUUGGCGAUAUAAGUAGGACGUGACCGAGGUGGAGACCUAGUGUGUGA 92
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
791 GATCAGATATCGAATTCGCCACCATGAGCTTCTTAACCGAGGTGCAAAACGTATGTTCT 850

Qy 93 GCAUACUCCCGAGCGGCCCGUGAAGCGCGAGAUCCGCCAGAGGUGGAGGACGUGUUG 152
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
851 CTATGCTTCATCAGGCCCCCTCAAGCCGAATCGGCGAGAGACTTGAAGATGTTCTTTG 910

Qy 153 CCGCAAGAACACCGACGUGAGUGUGUGAAGAGGUGGUGAAGACGAGGCCCAUCCUGA 212
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
911 CTGGGAAAACACAGATCTTGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCTCTGT 970

Qy 213 GCGCCUGACCAAGGGAUCCUGGGCUUGUGUUAUCCUGACCGUGGCCGAGCGCGCG 272
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
971 CACCTCTGACTAAGGGGATTTTGGGGTTTGTGTTTTCACGCTCACCGTGCAGAGTGAGCGAG 1030

Qy 273 GCUCGACGCGCGCGCUUGCGAGAACCGCCUGAACGCGCAACGCGGACCCCAACAACA 332
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1031 GACTGCGAGCTAGACGCTTTGTCCAAATGCCCTCAATGGGAATGGGGATCCAAATACAA 1090

Qy 333 UGGAACAAGGCGGUGAAGCUGUACAGGAAGCGUAGAGGAGGAGUACCUUCCACGCGCGCA 392
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1091 TGGACAGAGCATTAACACTATATAGAAAACCTTAAGAGGAGATTTACATTCCATGGGGCA 1150

Qy 393 AGGAGAUACGCCUGAGCUACAGCGCGCGCGCCUGGCGAGCUGCAUGGGCCUGAUUUA 452
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1151 AAGAAATAGCACTCAGTTATTCTGTGTGTCAGTTGCGCAGTTGATGCGGCTCATATACA 1210

Qy 453 ACAGGAUGGCGCGCGUACCAACCGAGGUGGCUUUGCGGUGGUGGCGCCACCGCGAGC 512
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1211 ACAGAAATGGGGCTGTAAACCACTGAATGGGCTTTTGGCCCTGTGTATGTGCAACATGTGAAC 1270

Qy 513 AGAUGCGCGCAGCAGCAGCACCGAGCCACAGGCGAGUAGUAGUACCAACCAACCCCGUGA 572
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1271 AGATTGCTGACTCCACAGCAGGTCTCATAGGCAAAATGGTGGCAACAACCAATCCATTAA 1330

Qy 573 UCAGGCAAGAGAACAGAUUGUGUGGCGCAGCACCAACCGCCCAAGGCGCAUGAGGAGU 632
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1331 TAAGGCATGAGAACAGAAATGGTTTGGCCAGCACTACAGCTTAAGGCTATGAGAGCAATGG 1390

Qy 633 CCGGCAAGGAGGCGCGCGAGCGCGAGGUGGAGGUGGCGAGCCAGCGCGAGGAGU 692
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1391 CTGGATCAAGTGAGCAGGCGAGGCGCATGGAAATTTGCTAGTCAAGGCGAGGCAATGG 1450

Qy 693 UGCAGGCGAUGAGGAGCAACUCCGCCACCCAGCGAGCGCGCGCGCGCGCAAGCAACGCC 752
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2006, 23:02:13 ; Search time 204.984 Seconds
(without alignments)
8767.110 Million cell updates/sec

Title: US-10-729-830-7
Perfect score: 1011
Sequence: 1 gcuugucuuuuugcagaag.....aaaaaaaaaaaaaaaaaaaaa 1011

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	479.6	47.4	4023	3	US-08-809-513A-8
2	479.6	47.4	4802	3	US-08-809-513A-6
3	477.6	47.2	1023	3	US-09-506-286B-1
4	477.6	47.2	1023	3	US-09-762-861B-1
5	477.6	47.2	1023	3	US-10-065-133A-1
6	477.6	47.2	1023	3	US-10-434-811A-1
7	477.4	47.2	816	3	US-09-311-784A-13
8	474.8	47.0	1023	3	US-09-506-286B-4
9	474.8	47.0	1023	3	US-09-762-861B-4
10	474.8	47.0	1023	3	US-10-065-133A-4
11	474.8	47.0	1023	3	US-10-434-811A-4
12	474.2	46.9	756	3	US-09-506-286B-3
13	474.2	46.9	756	3	US-09-762-861B-3
14	474.2	46.9	756	3	US-10-065-133A-3
15	474.2	46.9	756	3	US-10-434-811A-3
16	471.4	46.6	756	3	US-09-506-286B-6
17	471.4	46.6	756	3	US-09-762-861B-6
18	471.4	46.6	756	3	US-10-065-133A-6
19	471.4	46.6	756	3	US-10-434-811A-6
20	465.2	46.0	1027	6	PCT-US95-12357A-3
21	79.4	7.9	290	3	US-10-131-827-8418
22	79.4	7.9	1069	3	US-09-372-422A-7
23	79.4	7.9	1387	3	US-09-475-515-34
24	79.4	7.9	1944	3	US-09-475-515-37

25	79.4	7.9	1944	3	US-09-475-515-38	Sequence 38, Appl
26	79.4	7.9	1944	3	US-09-475-515-40	Sequence 40, Appl
27	79.4	7.9	1944	3	US-09-475-515-43	Sequence 43, Appl
28	79.4	7.9	1944	3	US-09-475-515-46	Sequence 46, Appl
29	79.4	7.9	2466	3	US-09-475-515-49	Sequence 49, Appl
30	79.4	7.9	4608	3	US-09-475-515-76	Sequence 76, Appl
31	79.2	7.8	2403	2	US-08-471-033-30	Sequence 30, Appl
32	79.2	7.8	2403	2	US-08-471-044-30	Sequence 30, Appl
33	79.2	7.8	2403	2	US-08-463-483A-30	Sequence 30, Appl
34	79.2	7.8	2403	2	US-08-471-046A-30	Sequence 30, Appl
35	79.2	7.8	2403	2	US-08-470-566B-30	Sequence 30, Appl
36	79.2	7.8	2403	2	US-08-838-219B-7	Sequence 7, Appl
37	79.2	7.8	2403	2	US-08-469-334-30	Sequence 30, Appl
38	79.2	7.8	2403	3	US-09-300-529-30	Sequence 30, Appl
39	79.2	7.8	2403	3	US-09-233-336A-7	Sequence 7, Appl
40	79.2	7.8	2403	3	US-09-233-752A-7	Sequence 7, Appl
41	79.2	7.8	2403	3	US-09-402-036-7	Sequence 7, Appl
42	79.2	7.8	2403	3	US-09-904-226-7	Sequence 7, Appl
43	77.6	7.7	1097	3	US-09-832-129-21	Sequence 21, Appl
44	77.6	7.7	2241	2	US-08-838-219B-20	Sequence 20, Appl
45	77.6	7.7	2241	3	US-09-233-336A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-809-513A-8
; Sequence 8, Application US/088095113A
; Patent No. 6524588
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
; TITLE OF INVENTION: Method
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NORRIS McLAUGHLIN & MARCUS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Gateway Pentium II
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,513A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03663
; FILING DATE: 18-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94115505.3
; FILING DATE: 30-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Hobom 9832-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4023 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

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; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Influenza virus, RNA sequence
; INDIVIDUAL ISOLATE: pHL1490
US-08-809-513A-8

Query Match 47.4%; Score 479.6; DB 3; Length 4023;
Best Local Similarity 65.2%; Pred. No. 7.2e-72;
Matches 494; Conservative 90; Mismatches 174; Indels 0; Gaps 0;

Qy 128 AGCUGUGACCGAGGUGGACCUAGUGUGAGAGCAUCCAGCGGCGCCCGCUAAG 187
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
21 AGTCTTCTAACCGAGGTGGAACGTAGTCTCTCTATCTCCGTAGGCCCCCTCAA 80
Qy |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
188 GCCGAGAUCCGCCAGAGCGUGAGGACGUGUUCGCCGCAAGAACACCGACCGUGAGUG 247
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
81 GCCGAGATCGCACAGAGACTTGAAGATGTCTTTGAGGGAAGAACCGATCTTGAGGTT 140
Qy 248 CUGAUGAGUGGUGAAGACAGCGCCNCCUUGAGCGCCCGCAGCAAGGCGUCCUGGCG 307
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
141 CTCATGGAATGGCTAAAGACAAAGACCAATCTCTGACCTGACTAAGGGGATTTAGGA 200
Qy 308 UUCGUGUACCCUGACCGUGCGCCAGCGAGCGCGCUGAGCGCCCGCGUUCUGUGCAG 367
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
201 TTTGTGTCAGCTCACCGTCCAGTGAGGAGACTGACGCTAGACGCTTTGTCAA 260
Qy 368 AACGCCCCUGAACCGGCAAGCGGCCCAACAAACUAGGACAAAGGCGCGUGAACGUGUACAGG 427
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
261 AATGCCCTTAATGGGAACGGGGATCCAAATAAATGAGCAAGCAAGTAAACTGTATAGG 320
Qy 428 AAGCUGAAGAGGAGAGACUUCUACGCGCGCGAGUACAAAGGAGUACGCGUAGCUACAGCGCC 487
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
321 AAGCTCAAGAGGAGATAACTTCCATGGGGCCAAAGAAATCTCACTCAATTTCTGCT 380
Qy 488 GCGCCCGUGGACGUGCAUGGCGCGUACUACAAAGAGUAGGCGCGUGACCAACCGAG 547
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
381 GGTGACTTGCAGTTGTATGGGCTCATATACACAGATGGGGCTGTGACCACTGAA 440
Qy 548 GUGGCCUUGGCGUGUGCGCCACCGUGAGCAGAUUGCGCAGCAGCAGCAGCCGAGC 607
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
441 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTTGCTACTCCAGCATCGGTCT 500
Qy 608 CACAGGCAUGGUGAGACACACACACCCCGUAGUACAGGCGCGAGAGAGAGAGUUGUGUG 667
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
501 CATAGGCAATGGTGACAAACCAACCAACCTAATACAGATGAGACAGAAATGGTTTA 560
Qy 668 GCCAGCACCGCCAGGCGCAUGGAGCAGAUUGGCGCGCAGCAGCGCGCGCGAG 727
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
561 GCCAGCACTACAGTTAAGGCTATGGAGCAATGGCTGATGAGTGAAGAGAGAGAG 620
Qy 728 GCCAUGGAGGCGCAGCCAGCGCCAGGAGUUGGUGAGGCGCAUGAGGACCAUUGCGCAC 787
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
621 GCCATGGAGGTTGTAGTCAGGCTAGGCAATGGTGAAGCGATGAGAACCATTTGGGACT 680
Qy 788 CACCCAGCAGCAGCGCCCGCGUAGAGACGACGUGUGGAGAACCUAGCGCCUACAG 847
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
681 CATCTTAGCTCCAGTGGTGTGAAAAAATGCTCTTTGAAAAATTTGCGAGGCTATCAG 740
Qy 848 AAGCGCAUGGCGUGCAUGCGCGUUCUAGUGAAC 885
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
741 AAACGATGGGGGTGCAGATGCAACGGTTCAAGTGATC 778

RESULT 2
US-08-809-513A-6
; Sequence 6, Application US/08809513A
; Patent No. 652458
; GENERAL INFORMATION:
; APPLICANT: Hobom, Gerd; Neumann, Gabriele; Menke, Annette
; TITLE OF INVENTION: An Attenuated Vaccination and Gene-Transfer Virus, a
; METHOD OF INVENTION: Method
; TITLE OF INVENTION: to Make the Virus and a Pharmaceutical Composition Comprising
; NUMBER OF SEQUENCES: 9
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Db 401 GGTGCACTTGGCAGTTGTATGGGCTCATATACAACAGGATGGGGCTGTGACCACTGAA 460
Qy 548 GUGGCUUGCGCTGUGUGUGCGCCACUGCGAGCAGAUUGCGCGCAGCCAGCCAGCGCAGC 607
Db 461 GTGGCAITTTGGCTGTGTATGTGCAACCTGTGAACAGATTGTGACTCCAGCATCGTCT 520
Qy 608 CACAGGCAUGUGUGACACCAACCAACCCUUGAUCAGGCAACGAGAAACAGGAUGUGUG 667
Db 521 CATAGGCAATGGTGACAAACCAACCAACCACTAATCAGACATGAGAACAGAAATGTTTA 580
Qy 668 GCGAGCACCGCCAGGCAUGAGCAGGAUGGCGCGCAGCAGGAGCGCGCCGAG 727
Db 581 GCGAGCACTACAGCTAAGGCTATGGAGCAATGGCTGATCGAGTGAGCAAGCAGCAG 640
Qy 728 GCCAUGGAGUGGCGCAGCCAGCCAGGCAUGGUGUGAGGCAUGAGCAACCAUGCGCAC 787
Db 641 GCCATGGAGGTTGTAGTCAGGCTAGGCAATGGTGACGATGAGAACCTTTGGGACT 700
Qy 788 CACCCCAAGCAGCGCGCCUGAAGAACCAACCUUGUGGAGAACCUUGCAGGCCUACCA 847
Db 701 CATCTAGCTCCAGTGTGTCTGAAATAATGCTCTCTTTGAAATTTTGCAGGCTATCAG 760
Qy 848 AAGCGCAUGGCGUGCAGAUAGCAGCGCUUCAAAGUGAAC 885
Db 761 AAACGAATGGGGTGCAGATGCAACGGTTCAAGTGATC 798

RESULT 3

US-09-506-286B-1
; Sequence 1, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: The University of Pittsburgh, of the Commonwealth
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION: At location 663, r = A or G; At amino acid
; OTHER INFORMATION: location 213, Xaa = Val
US-09-506-286B-1

Query Match 47.2%; Score 477.6; DB 3; Length 1023;
Best Local Similarity 65.0%; Fred. NO. 1.3e-71;
Matches 493; Conservative 90; Mismatches 175; Indels 0; Gaps 0;

Qy 128 AGCCUGUGACCGGAGUGGAGACCUACGUGUGAGCAUCAUCCCGCGGCCCGCUGAAG 187
Db 28 AGTCTTCTGACGAGGTGCAACGTAAGTCTCTCTATCTGTAACATCAGGCCCTCTCAA 87
Qy 188 GCCGAGUCCGCCAGGCGUGGAGACGUGUUCGCCGCAAGAACCCAGCUGGAGUG 247
Db 88 GCCGAGATCGCGAGAGACTTGAAGATGCTTTTGCAGGGAAGAACACCGATCTTTAGGCA 147
Qy 248 CUGAUGGAGUGGCTUGAAGACAGCGCCCAUCCUGAGCCCGCUGACCAAGGGCAUCCUGGC 307
Db 148 CTCATGGAATGGCTAAAGACAAGAACCAATCTGTCTGTCTGACTTAAGGATTTTAGGA 207
Qy 308 UUCGUGUACCCUGACCGUGCCCGCAGCGCGCCUGCAGCGCGCGCGCUGUGCAG 367

Db 208 TTGCTATTACGCTCACCGTGCCAGTGAGCGAGGACTGCAGCGGTAGACGCTTTGTCAA 267
Qy 368 AAGCCCUAGAACCGCAACCGGACCCCAACAACUAGGACAGCCCGUGAAGCUGUACAGG 427
Db 268 AATGCCCTTATGTGAAACCGGAGATCCAAACAACATGGACAGAGCAGTAACACTGTACAGG 327
Qy 428 AAGCUGAAGAGGAGAUCAACCUCCACGCGCCCAAGAGAGAUCAAGCCUGAGCUCACAGGCC 487
Db 328 AAGCTTAAAGAGAAATAACATTTCCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 387
Qy 488 GCGCCCUUGCGCCAGCUGCAUGGCGCUUACUACAACAGGAUGGCGCGCUGACCAACCGAG 547
Db 388 GGTGCACTAGCCAGCTGCTGGGACTCATATACAACAGAAATGGGAACCTGTGACAAACGAA 447
Qy 548 GUGGCCUUGCGCGUGUGUGCGCACCUUGAGCAGAUCCGCCACACAGCAGCAGCAGCCGAGC 607
Db 448 GTGCAATTTGGCCTGTGTATGCGCCACATGTGAACAGATCCGTATTTCCAGCATCGATCT 507
Qy 608 CACAGGCAUGUGUACCAACCAACCCUUGAUCAGGCAACGAGGCAACAGAGUUGUGUG 667
Db 508 CACAGGCAUGTGTGACAAACAACCCATTAATCAGACATGAANAACAGAAATGTTATTA 567
Qy 668 GCGAGCACCAACCGCAAGGCAUGGAGCAGAUUGGCGCGCAGCAGCGAGCGCCGAG 727
Db 568 GCCAGTACCACCGCTAAAGCCATGGAGCAGATGCGAGGGTCTGAGTGAGCAGGCGAGCAG 627
Qy 728 GCCAUGGAGUGGCGCAGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 787
Db 628 GCCATGGAGTTTCTAGTAAGGCTTAGCAGATGTRCAGGCAATGAGAACCATTTGGGACC 687
Qy 788 CACCCCAAGCAGCAGCGCGCGCUGAAGAACGACCUUGCUGGAGAACCUUGCAGGCUACAG 847
Db 688 CACCTAGCTCCAGTGGCGGTTTGAAGATGATCTCTCTGAAATTTGCGAGGCTTACAG 747
Qy 848 AAGCGCAUGGCGUGGAGUAGCAGCGCUUCAAAGUGAAC 885
Db 748 AAACGATGGGAGTGCAATGCAAGGATTCAGATGATC 785

RESULT 4

US-09-762-861B-1
; Sequence 1, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS (formerly HK2-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-09-762-861B-1

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Query Match      47.2%; Score 477.6; DB 3; Length 1023;
Best Local Similarity 65.0%; Pred. No. 1.3e-71;
Matches 493; Conservative 90; Mismatches 175; Indels 0; Gaps 0;

Qy 128 AGCCUGUGACCGAGGUGGAGACCUAGUGUGAGCAUACUCCAGCGGCCCGCCUGAAG 187
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Db 28 AGTCTTCTGACCGAGGTGGAACGTAGCTTCTCTATCGTACCATCAGGCCCTTCAA 87
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Qy 188 GCCGAGAUCCCGCCAGGAGGAGCGUGUUCGCCGCGCAAGAACACCGCUGGAGUG 247
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Db 88 GCCGAGATCGCGAGAGACTTGAAGTGTCTTTGCGAGGAGAACCGGATCTTGAGGCA 147
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Qy 248 CUGAUGAGUGGUGUAGAGACAGCGCCCAUCCUGAGCGCCUGACCAAGGGCAUCCUGGC 307
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 148 CTCATGGAATGGCTAAGACAGACCACTCTCTGACTGACTAAGGGATTTAGGA 207
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 308 UUCGUGUACCCUGACCGUGCCAGCGAGCGCGCCUGCAGCGCCCGCGUUGUGCAG 367
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 208 TTCGTATTTCAGCTCACCGTCCCGAGTGAGCGAGACTGCGAGCGTGTGTCGAA 267
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 368 AACGCCCCUGAACCGGCAACCGCGACCCCAACCAUUGGACAGGCGCGUGAAGCUGUACAGG 427
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 268 AATGCCCTTAGTGGAAACGAGATCCAAACAACTGACGAGCAGTAAACTGTACAGG 327
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Qy 428 AAGCUGAAGAGGAGAGUACCUUCCAGCGCCCAAGGAGAUACGCCUGAGCUACAGCGCC 487
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Db 328 AAGCTTAAAGAGAAATAACATTCCATGGGCAAAAGAGGTGGCACTATTTCCACT 387
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Qy 488 GCGCGCCUGGCGACUGCGGCGUGAUCUACACAGAGAGUGGCGCGUGACCAACCGAG 547
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Db 388 GGTGCACTAGCCAGCTGCATGGGACTCATATACACAGAAATGGGAACTGTGACAAACGAA 447
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Qy 548 GUGCGCUUCCUGGUGUGCGCCACCGAGCAGAGUUGCGCGCAGCCAGCCGCGAGC 607
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Db 448 GTGGCATTTGGCTTGGTATGGCCACATGTGAAACAGATCGTGTATCCAGCATCGATCT 507
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Qy 608 CACAGGCGAUGUGUAGACCAACCAACCGCCUGAUCAGGCGACGAGAACCAUCCGCAAC 667
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Db 508 CACAGGCGATGTGTAGTAAAGCTAGGCTAGGCGATGTRCAGGCAATGAGAACCATTTGGGACC 687
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Qy 788 CACCCGACGACGCGCGCGUGAAGAACCAUCCUGUGGAGAACUCCUGAGCGCCUACAG 847
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Qy 848 AAGCGCAUGGCGUGCAGUACGCGGCUUACAGUAGAAC 885
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RESULT 5

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US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
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; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, xaa = Val
US-10-065-133A-1
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Query Match      47.2%; Score 477.6; DB 3; Length 1023;
Best Local Similarity 65.0%; Pred. No. 1.3e-71;
Matches 493; Conservative 90; Mismatches 175; Indels 0; Gaps 0;

Qy 128 AGCCUGUGACCGAGGUGGAGACCUAGUGUGAGCAUACUCCAGCGGCCCGCCUGAAG 187
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Db 28 AGTCTTCTGACCGAGGTGGAACGTAGCTTCTCTATCGTACCATCAGGCCCTTCAA 87
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Qy 188 GCCGAGAUCCCGCCAGGAGGAGCGUGUUCGCCGCGCAAGAACACCGCUGGAGUG 247
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Db 88 GCCGAGATCGCGAGAGACTTGAAGTGTCTTTGCGAGGAGAACCGGATCTTGAGGCA 147
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Qy 248 CUGAUGAGUGGUGUAGAGACCGCGACCCCAACCAUUGGACAGGCGCGUGAAGCUGUACAGG 427
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Db 148 CTCATGGAATGGCTAAGACAGACCACTCTCTGACTGACTAAGGGATTTAGGA 207
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Qy 308 UUCGUGUACCCUGACCGUGCCAGCGAGCGCGCCUGCAGCGCCCGCGUUGUGCAG 367
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Qy 368 AACGCCCCUGAACCGGCAACCGCGACCCCAACCAUUGGACAGGCGCGUGAAGCUGUACAGG 427
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Qy 428 AAGCUGAAGAGGAGAGUACCUUCCAGCGCGCCCAAGGAGAUACGCCUGAGCUACAGCGCC 487
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Db 328 AAGCTTAAAGAGAAATAACATTCCATGGGCAAAAGAGGTGGCACTATTTCCACT 387
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Qy 488 GCGCGCCUGGCGACUGCGGCGUGAUCUACACAGAGAGUGGCGCGUGACCAACCGAG 547
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Db 388 GGTGCACTAGCCAGCTGCATGGGACTCATATACACAGAAATGGGAACTGTGACAAACGAA 447
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 548 GUGCGCUUCCUGGUGUGCGCCACCGAGCAGAGUUGCGCGCAGCCAGCCGCGAGC 607
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 448 GTGGCATTTGGCTTGGTATGGCCACATGTGAAACAGATCGTGTATCCAGCATCGATCT 507
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Qy 608 CACAGGCGAUGUGUAGACCAACCAACCGCCUGAUCAGGCGACGAGAACCAUCCGCAAC 667
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Db 508 CACAGGCGATGTGTAGTAAAGCTAGGCTAGGCGATGTRCAGGCAATGAGAACCATTTGGGACC 687
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Qy 788 CACCCGACGACGCGCGCGUGAAGAACCAUCCUGUGGAGAACUCCUGAGCGCCUACAG 847
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Qy 848 AAGCGCAUGGCGUGCAGUACGCGGCUUACAGUAGAAC 885
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Db 748 AAACGGATGGGAGTGCAAAATGCGAGGATTTCAAGTGATC 785
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[illegible]

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, CURRENT FILING DATE: 1999-05-13
, PRIOR APPLICATION NUMBER: US 60/085,751
, PRIOR FILING DATE: 1998-05-15
, NUMBER OF SEQ ID NOS: 463
, SOFTWARE: FastSeq for Windows Version 3.0
, SEQ ID NO 13
, LENGTH: 816
, TYPE: DNA
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
, OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of
, OTHER INFORMATION: influenza matrix protein gene
, NAME/KEY: CDS
, LOCATION: (16) ... (816)
, OTHER INFORMATION: PADRE-Influenza matrix
US-09-311-784A-13

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Query Match	47.2%	Score	477.4	DB 3	Length	816
Best Local Similarity	64.4%	Pred. No.	1.4e-71			
Matches	504	Conservative	88	Mismatches	191	Indels
					0	Gaps
					0	
Qy	101	GCCTCGCCCGACCCAGACCCUGGGCCAGCTGUCAGCCGAGGUGGAGAGACCAUACGUGCUG	160			
Db	34	GCCTGACCCCTGAAGGCTGCCGTATGAGTCTCTTAACCGAGGTGCGAATCGATGCTCTC	93			
Qy	161	AGCAUCAUCCCGACGGCCCCCUGAAGGGCCGAGAUCCGCCAGGCGUGGAGGACGUGUUC	220			
Db	94	TCTATCATCCCATCAGGCCCCCTCAAAGCCGAGATCGCGCAGAGACTTGAGGATGTTTT	153			
Qy	221	GCGCGCAAGAACACCGACCTUGGAGGUGUCUGAUGGAGUGGCGUGAAGACCGAGGCCCAUCCUG	280			
Db	154	GCAGGGAAGAACACAGATCTTGAGGCTCTCATGGAAATGGCTAAAGACAAGACCAATCCTG	213			
Qy	281	AGCCCCCUGACCAAGGGCAUCCUGGCUUGUGUUCACCCUGACCCUGGCCACCGAGCGC	340			
Db	214	TCACTCTGACTAAGGGAATTTTAGGTTTGTGTTTCAACGCTACCGTGCCTAGTGAGCGA	273			

341	Qy	GGCCUGAGCGCCGCGUUCUGAGAAACGCCUGAAACGGCAACGCCCAACAAAC	400
342		: :	
274	Db	GGATGACGGGTAGACGATTGTTCCAAATGCGCTTAAATGGGAATGGAGACCCAAACAAAC	333
275		: :	
401	Qy	AUGGACAAGCCGUGAAGCUGUACAGGAAGCUGAAGAGGGAGAUACACCUCCACGGCGCC	460
402		: :	
334	Db	ATGACAGGGCAGTTAAACTATACAAGAAGCTGAAGAGGGAATGACATTCCATGGAGCA	393
335		: :	
461	Qy	AAGGAGAUACAGCUGAGCUACAGCGCCGCGCCUUGGCCAGCUGCAUGGGCGCUGAUCUAC	520
462		: :	
394	Db	AAGGAAGTTGCACCTCAGTTACTCAACTGSGTGGCTTGCCAGTTGCTGGTCTCATATAC	453
395		: :	
521	Qy	AACAGGAUGGGCGCGUGAACACCGAGUGGCGUUCGGCCUGUGUGGCCACACUCCUGCGAG	580
522		: :	
454	Db	AACCGGATGGGAACAGTGACACCAAGATGGGCTCTTGGCCCTAGTATGTGCCACTTGTGAG	513
455		: :	
581	Qy	CAGAUCCCGACAGCCAGCACCGCAGCCACAGGAGAGUGGUGACCAACCAACCCCCUG	640
582		: :	
514	Db	CAGATTGCTGATGCCCAACATCGGTGCCACAGGCAGATGGCGGACTACCAACCAACCACTA	573
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641	Qy	AUCAGGCACAGAAACAGGAUGGUGUGGCCAGCACACCGGCCAAGGCCAUGAGAGCAGAUG	700
642		: :	
574	Db	ATCAGGCATGAGAACAGAAATGGTACTAGCCAGCACTACGGCTAAGGCCATGGAGCAATG	633
575		: :	
701	Qy	GCGGCGAGCAGCAGCGGCCGCGAGGCCAUGAGGUGGCCAGCCAGGCCAGGCGAGAUG	760
702		: :	
634	Db	GCTGGATCAAGTGAGCAGGCAGCAGAGGCCATGGAAGTCGAAAGTCAGGCTAGACAAATG	693
635		: :	
761	Qy	GUGCAGGCCAUGAGGACAUCAGGCGACCCACCCAGCAGCGCGCGCCUGAAGAACGAC	820
762		: :	
694	Db	GTGCAGGCAATGAGAGCAATTTGGGACTCACCCCTAGCTCCAGTGCAGGTTCTAAGATGAT	753
695		: :	
821	Qy	CUGCUGAGAAACCUCCAGCGCCUACACAGAAGCGCAUGGGCGUGCAGUGCAGCGCCUUCAG	880
822		: :	
754	Db	CTTATTGAAATTTGCGGCCTTACAGAAAACGATGGGGTGCAGATGCAGCGATTCAG	813
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881	Qy	UGA 883	
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814	Db	TGA 816	
815			

RESULT 8

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US-09-506-286B-4
; Sequence 4, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (25) .. (780)
; US-09-506-286B-4

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[illegible]


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Qy 608 CACAGGAGAGUGGUGACCAACACACCCUUGAUCAGGACGAGAACAGGAGUGUG 667
Db 484 CACAGGAGATGGTGACAAACCAACCAACCATTAATCAGACATGAACAGATGATTA 543
Qy 668 GCCAGCACCCGCGCAAGGCGUAGGAGCAGUGGCGGCGAGCAGGAGCGCGCCGAG 727
Db 544 GCCAGTACACGGCTAAAGCCATGGAGCAGATGGCAGGTCGAGTGAGCAGGACGAG 603
Qy 728 GCCAUGGAGUGGCGCAGGCGCAGGAGGUGGAGGUGGAGGAGGAGGAGGAGGAGG 787
Db 604 GCCATGGAGGTTGCTAGTAAGGCTAGGAGCAGATGGTTCAGGCAATGAGAAACCA 663
Qy 788 CACCCAGCAGCAGCGCGCGCGUAGGAGCAGCAGCUGUGGAGGAGGAGGAGGAGG 847
Db 664 CACCCAGTCTCAGTGCCTGGTTTGAAGATGATCTCTTGAATAATTTGAGGCTTAC 723
Qy 848 AAGCGCAUGGCGUGAGCAGGAGGCGGCGUUCUUAAG 880
Db 724 AACCGATGGGAGTGCAAAATGCAGGATTCAAG 756
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RESULT 13

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US-09-762-861B-3
; Sequence 3, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-CL-PUS (formerly HKZ-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-762-861B-3
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Query Match 46.9%; Score 474.2; DB 3; Length 756;
Best Local Similarity 65.1%; Pred. No. 4.7e-71;
Matches 490; Conservative 89; Mismatches 174; Indels 0; Gaps 0;

Qy 128 AGCCUGUGACCCGAGGUGGAGACCUAGUGUGGAGGAGGAGGAGGAGGAGGAGG 187
Db 4 AGTCTTCTGACCGAGGTCGAAACGTAAGTCTCTCTATCGTACCATCAGGCCCCCTCAA 63
Qy 188 GCCGAGAUCCCGGAGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 247
Db 64 GCCGAGATCGCGAGAGACTTGAAGATGTCTTTGAGGGAAGAACACCGATCTTGAGGCA 123
Qy 248 CUGAUGAGUGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 307
Db 124 CTCATGGATGGCTTAAGACAGACCAATCTCTGATCTGATTAAGGATTTTAGGA 183
Qy 308 UUCGUGUUAUCCUGACCGGCGCCAGCGAGGCGCGGCGGCGGCGGCGGCGGCGG 367
Db 184 TTCGTATTACGCTCACCGTCCCGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 243
Qy 368 AACGCCUGAAGCGGCAACCGGCGCCCAACAAACAGGAGGAGGAGGAGGAGGAGG 427
Db 244 AATGCCCTTAGTGGAAACGGAGATCCAAACAAACATGGAAGAGGAGGAGGAGGAGG 303
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Qy 428 AAGCUGAAGAGGAGGAGAUCAUCCUACCGCGCCCAAGGAGAGAUCAUCCUGAGCUACGAGCC 487
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Db 364 GGTGCACTAGCCAGCTCATATACAAAGAAATGGGAATGTGTACAAACCGAA 423
Qy 548 GUGGCUUUGCGCGUGUGUGCGCCACUUGCGAGCAGAUCCGCCGAGCAGCAGCAGCAGCAGC 607
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Qy 608 CACAGGAGAGGUGAGCACACCAACCCUUGAUCAGGAGGAGGAGGAGGAGGAGGAGGAGG 667
Db 484 CACAGGAGATGGTGACAAACCAACCAACCCATTAAATCAGACATGAACAGAAATGGTA 543
Qy 668 GCCAGCACCCGCGCAAGGCGGCGGCGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGG 727
Db 544 GCCAGTACCAACCGGCTAAAGCCATGGAGCAGATGGCAGGTCGAGTGAGCAGGAGCAGAG 603
Qy 728 GCCAUGGAGUGGCGCAGGCGCAGGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 787
Db 604 GCCATGGAGGTTGCTAGTAAGGCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 663
Qy 788 CACCCAGCAGCAGCGCGCGCGGCGGCGGCGGAGCAGCAGCAGCAGCAGCAGCAGCAG 847
Db 664 CACCCAGTCTCAGTGCCTGGTTTGAAGATGATCTCTCTTGAATAATTTGAGGCTTAC 723
Qy 848 AAGCGCAUGGCGUGAGCAGGAGGCGGCGUUCUUAAG 880
Db 724 AACCGATGGGAGTGCAAAATGCAGGATTCAAG 756
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RESULT 14

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US-10-065-133A-3
; Sequence 3, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-3
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Query Match 46.9%; Score 474.2; DB 3; Length 756;
Best Local Similarity 65.1%; Pred. No. 4.7e-71;
Matches 490; Conservative 89; Mismatches 174; Indels 0; Gaps 0;

Qy 128 AGCCUGUGACCCGAGGUGGAGACCUAGUGUGGAGGAGGAGGAGGAGGAGGAGG 187
Db 4 AGTCTTCTGACCGAGGTCGAAACGTAAGTCTCTCTATCGTACCATCAGGCCCCCTCAA 63
Qy 188 GCCGAGAUCCCGGAGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 247
Db 64 GCCGAGATCGCGAGAGACTTGAAGATGTCTTTGAGGGAAGAACACCGATCTTGAGGCA 123
Qy 248 CUGAUGAGUGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 307
Db 124 CTCATGGATGGCTTAAGACAGACCAATCTCTGATCTGATTAAGGATTTTAGGA 183
Qy 308 UUCGUGUUAUCCUGACCGGCGCCAGCGAGGCGCGGCGGCGGCGGCGGCGGCGG 367
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Db      184  TTGTAATTCACGCTACCGTCCAGTGGAGGAGTGCAGCTAGACGCTTTGTCAA 243
Qy      368  AACGCCUUGAAGCGCAACCGCGACCCCAACAAACUUGGACAAAGGCGGUGAAGCUUACAGG 427
Db      244  AATGCCCTTAGTGGAAACGGAGATCCAAACAACATGGACAGAGCAGTAATAACTGTACAGG 303
Qy      428  AAGCUGAAGAGGAGAUCAACUUCACGCGCCGCAAGGAGAUCAAGCCUGAGCUACAGCGCC 487
Db      304  AAGCTTAAAGAGAAATAACATTCATGGGGCAAAAGAGGTGGCACTCAGCTATTCCACT 363
Qy      488  GGCGCCUUGGCGAGCUGAUGGCGGCUUACUACACAGAGGAGGCGGCGGUGACCAACCGAG 547
Db      364  GGTGCATAGGCGAGCTGCATGGGACTCATATACAAACAGATGGGAACTGTGACAAACGAA 423
Qy      548  GUGGCCUUGGCGGUGUGCGCCACCGCAGCAGAGUUGCGCGACAGCGCAGCAGCGCAGC 607
Db      424  GTGGCATTTGGCTGGTATGGCCACATGTGAACAGATCGTGTATCCAGCATCGATCT 483
Qy      608  CACAGGCGAUGGUGUACACCAACCAACCCUUGAUCAGGCGACGAGAACAGGAUGGUGUG 667
Db      484  CACAGGCGAGTGGTGACAAACCAACCAACCAATTAATCAGACATGAAACAGAAATGGTATTA 543
Qy      668  GCCAGCACCGCGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 727
Db      544  GCCAGTACCGCGCTAAAGCCATGGAGCAGATGGCGGCTCGATGGAGCGGCGGCGGCGG 603
Qy      728  GCCAUGAGGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 787
Db      604  GCCATGGAGGTGTAGTAAGCTTAGCGGCTTGAAGATGATCTCTTGAATAATTTGCAGGCC 663
Qy      788  CACCCCGACAGCAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 847
Db      664  CACCCCTAGCTCAGTGCAGGCGGTTTGAAGATGATCTCTTGAATAATTTGCAGGCC 723
Qy      848  AAGCGCAUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 880
Db      724  AAACGGATGGGAGTGCAAAATGACGGATTCAAG 756

RESULT 15
US-10-434-811A-3
; Sequence 3, Application US/10434811A
; Patent No. 6824784
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-434-811A-3
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Query Match 46.9%; Score 474.2; DB 3; Length 756;
Best Local Similarity 65.1%; Pred. No. 4.7e-71;
Matches 490; Conservative 89; Mismatches 174; Indels 0; Gaps 0;

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Qy      128  AGCCUGUACCGGAGGAGGAGACCUACGUGUGAGAGCAUCCCGGCGGCGGCGGCGGCGG 187
Db      4   AGTCTTCAGCCGAGGTGAAACGTACGTTCTCTATCGTACCACGAGGCGGCGGCGG 63
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Search completed: March 20, 2006, 23:50:30
Job time : 207.984 secs

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Qy      188  GCCGAGAUCCGCCAGAGGCGUGGAGGAGCGUUCUUCGCGCGCAAGAACACCGACCGGAGGUG 247
Db      64   GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTTCAGGGGGAAGAACACCGGATCTTGAGGCA 123
Qy      248  CUGAUGGAGUGGUGUGAAGACACAGCGCCCAUCUUGAGGCGCCUGAGCCCAAGGCGCAUCCUGGGC 307
Db      124  CTCATGGATGGCTAAAGACACAGCCAACTCTCTCCTCTGACTAAGAGGATTTAGGA 183
Qy      308  UUCGUGUACACCGUACCGUGCGCAGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 367
Db      184  TTCGTATTACGCTCACCGTCCCGTCCAGTGAGCGAGGAGTGCAGCGGTAGACGCTTTGTCAA 243
Qy      368  AAGCGCCUUGAACCGGCAACCGCGACCCCAACAAUUGGACAGGCGGCGGCGGCGGCGGCGGCGG 427
Db      244  AATGCCCTTAGTGGAAACCGGAGATCCAAACCAATGGACAGAGCAGTAAACCTGTACAGG 303
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Db      304  AAGCTTAAAGAGAAATTAATTCATGGGCGGCAAAAGAGGTGGCACTCAGCTATTCCACT 363
Qy      488  GGCGCCUUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 547
Db      364  GGTGCATAGCAGCTGCGTGGGACTCATATACAAACAGAAATGGGAACTGTGACAAACGAA 423
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Db      424  GTGGCATTTGGCTGGTATGGCCACATGTGAACAGATCGCTGATTTCCAGCATCGATCT 483
Qy      608  CACAGGCGAUGGUGUACCAACCAACCCUUGAUCAGGCGACGAGAACAGGAUGGUGUGUGUG 667
Db      484  CACAGGCGAGTGGTGACAAACCAACCAACCCATTAATCAGACATGAAACAGAAATGGTATTA 543
Qy      668  GCCAGCACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 727
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Qy      728  GCCAUGAGGUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 787
Db      604  GCCATGGAGGTGTCTAGTAAGGCTTAGCGGCTTGAAGATGATCTCTTGAATAATTTGCAGGCC 663
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Db      664  CACCCCTAGCTCAGTGCAGGCGGTTTGAAGATGATCTCTTGAATAATTTGCAGGCC 723
Qy      848  AAGCGCAUGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 880
Db      724  AAACGGATGGGAGTGCAAAATGACGGATTCAAG 756
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QY 241 GGAGGUCUGAGGAGUGGUGAAGACAGCGCCCAUCUGAGCGCCCGUAGACCAAGGGCAU 300
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QY 301 CCUGGGCUUGGUGUUCACCCUGACCGUGCCAGCGAGCGGCGCUGCAGCGCCCGCUU 360
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|
|
Db 301 CCUGGGCUUGGUGUUCACCCUGACCGUGCCAGCGAGCGGCGCUGCAGCGCCCGCUU 360
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|
|
QY 361 CGUGCAGAACCGCCUGAACCGGCAACGGCGACCCCAACAAUGACAAAGGCCUGAAGCU 420
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Db 361 CGUGCAGAACCGCCUGAACCGGCAACGGCGACCCCAACAAUGACAAAGGCCUGAAGCU 420
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|
|
QY 421 GUACAGGAAGCUGAAGAGGAGAUCAUCUCCAGCGGCCCAAGGAGAUACGCGUGAGCUA 480
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Db 421 GUACAGGAAGCUGAAGAGGAGAUCAUCUCCAGCGGCCCAAGGAGAUACGCGUGAGCUA 480
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|
|
QY 481 CAGCGCGCGCGCCUGGCGCAGCUGCAUGGGCCUGAUCAACAGGAGUGGGCGCGGUGAC 540
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QY 841 CUACCAAGCGCAUGGCGCGUGCAGAGCAGCGCUUCAAGUGAACUAGUGACUAGC 900
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QY 901 CCGCUGGGCCUCCCAACGGGCGCUCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCU 960
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Db 901 CCGCUGGGCCUCCCAACGGGCGCUCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCUCCU 960
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US-10-729-830-6
; Sequence 6, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
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; SOFTWARE: PatentIn Ver. 2.1.1
; SEQ ID NO 6
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA with increased G/C-content and
; OTHER INFORMATION: stabilisation sequences
; FEATURE:
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
; OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-6

Query Match      87.4%; Score 884; DB 8: Length 942;
Best Local Similarity 100.0%; Pred. No. 1.2e-168;
Matches 884; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 188 GCCAGAUCCCGCAGAGGCGUGAGGACGUGUUGCGCGGCAAGAACACCGACCUUGGAGGUG 247
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Db 119 GCCAGAUCCCGCAGAGGCGUGAGGACGUGUUGCGCGGCAAGAACACCGACCUUGGAGGUG 178
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QY 428 AACGUCNAGGAGGAGAUCAUCCUACCGCGGCCCAAGAGAUACGCGUGAGCUACAGCGCC 487
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QY 548 GUGGCGCUUGGCGCGUGUGCGCGCACCGUGCGAGCAGAUCCGCCAGCAGCGACCGCGCAGC 607
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Db 479 GUGGCGCUUGGCGCGUGUGCGCGCACCGUGCGAGCAGAUCCGCCAGCAGCGACCGCGCAGC 538
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QY 608 CACAGCGAGUUGGAGGACCAACCGCGCGCGUGAAGCGCGCGCGCGCGCGCGCGCGCGCG 667
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QY 668 GCCAGCACCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727
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Db 599 GCCAGCACCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 658
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QY 728 GCCAUGGAGUGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 787
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Db 659 GCCAUGGAGUGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 718
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Db 719 CACCGCAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 778
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QY 308 UUCGUGUUCACCCUGACCGGCGCCAGGAGCGCGCCUGCAGCGCCCGCCGCGUGUGCAG 367
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QY 428 AAGCUGAAGGAGGAUACUUCUACCGCGGCAAGGAGAGUACAGCUGAGCUACAGCGCC 487
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314 AAGCTGAAGAGGGAGATCACTTCCAGCGCGCCAAAGGAGATCAGCCTGAGCTACAGCGCC 373
QY 488 GGCGCCCTGCGCAGCUGCAUGGGCGUGAUCUACAAACAGGAUGGGCGCGCGUGACCAACCGAG 547
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374 GGCGCCCTGCGCAGCTGATGGGCTGATCTACAAAGGATGGCGCGGTGACCAACCGAG 433
QY 548 GUGGCCUUGGCGCUGUGUGGCGCACUUGCGAGCAGAUUCGCGAGACGCCAGCAGCGCAGC 607
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
434 GTGGCCTTGGCCTTGGTGTGGCCACCTTGGAGCAGATCGCCGACAGCCAGCAGCAGCGCAGC 493
QY 608 CACAGGCGAGUGGUGACCAACCAACCCCTUGAUCAGGACGAGACAGAGAGGUGGUGCUG 667
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
494 CACAGGCGAGATGGTGACCAACCAACCCCTGTATCAGGACGAGAACAGATGGTGTCTG 553
QY 668 GCCAGCACCAACCGCAAGGCGCAUGGAGCAGAUAGCGCGCGCAGCAGCAGCGCGCGCGAG 727
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
554 GCCAGCACCAACCGCAAGGCGCATGAGCAGATGCGCGCGCAGCAGCAGCGCGCGCGAG 613
QY 728 GCCAUGAGGUGGCGCACCGCAGGCGCAGCAGAUUGGUGCAGGCGCAUGAGGACCAUCGGCACC 787
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
614 GCCATGAGGTGGCGAGCCAGGCGCAGCAGATGCTGAGGCGCATGAGGACCATCGGCACC 673
QY 788 CACCCGAGCAGCAGCGCGCGCGCUAGAACGACCTUGGAGAACCTUGCAGGCGCUACAG 847
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
674 CACCCGAGCAGCAGCGCGCGCTGAAGAACGACCTGTGTGAGAACCTGCGAGGCGCTACCG 733
QY 848 AAGCGCAUGGCGUGCAGAUAGCAGCGCUUCAAGGAAACUAGU 889
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
734 AAGCGCATGGCGTGCAGATGACGCGCTTCAAGTGAACCTAGT 775
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RESULT 5
US-10-729-830-5
; Sequence 5, Application US/10729830
; Publication No. US2005003730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; TITLE OF INVENTION: Optimised for translation in its coding regions
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; PRIOR FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 942
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Influenza
; OTHER INFORMATION: matrix: mRNA with stabilisation sequences
; FEATURE:
; OTHER INFORMATION: The stabilisation sequences are derived from 5'-
; OTHER INFORMATION: and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
; OTHER INFORMATION: respectively.
```

```
; FEATURE:
; OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
; OTHER INFORMATION: codon: uga (nucleotides 812 to 814)
US-10-729-830-5

Query Match 60.2%; Score 608.8; DB 8; Length 942;
Best Local Similarity 80.5%; Pred. No. 3.6e-113;
Matches 712; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

QY 128 AGCCUGCUGACCGAGGUGGAGACCUACGUGCTUGAGCAUCAUCCCGCAGCGCCCGCCUGAAG 187
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
59 AGUCUUCUAAACCGAGGUCGAAACGUAAGUUCUCUAUCCGUCAGCGCCCGCCUCAA 118
QY 188 GCCGAGAUCCCGCAGAGGCGUGGAGGAGUUCGCGCGCAAGAACACCGACCUUGGAGGUG 247
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
119 GCCGAGAUCCGACAGAGACUUGAAGUUCUUGAGGAGGAGAACCCGCAUUCUAGGUU 178
QY 248 CUGAUGGAGUGGUGGAGAGACCAAGCGCCCAUUCUGAGCGCCUGACCAAGGCGCAUCCUGGGC 307
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
179 CUCUAGGAUUGCUAAAGACNAGACCAUCCUGUACCUUGACUAAGGGAUUTUAGGA 238
QY 308 UUCGUGUUCACCCUGACCGGCGCCAGCGAGCGCGCGCUGCAGCGCGCGCGCUGUGCAG 367
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
239 UUUUGUUCACGUCUACCGGCGCGCAGUGAGCGAGGACUGCAGCGUAGACGCUUUGCCAA 298
QY 368 AACGCCUGAACCGCAACCGCGACCCCAACAAUCAGGACAAAGCGCGUGAAGCUUACAGG 427
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
299 AAGCGCCUUAUAGGGAAACGGGGAUCCAAUAACAUGGACAAAGCAGUUAACUUGUAUAGG 358
QY 428 AAGCUGAAGGAGAGAUACACUUCACCGCGCGCAAGGAGAUACAGCCUGAGCUACAGCGCC 487
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
359 AAGCUCAGAGGAGAUACAUAUCCAUUGGGCGCAAGAAAUUCACUCAGUUAUUCUGCU 418
QY 488 GCGCGCCUGCGCAGCUGCAUGGCGCUAUCACAAAGAGUAGGCGCGCGUGACCAACCGAG 547
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
419 GGUGCAUUGGCCAGUUGUAGUGGCGCUCAUAUACAAGAGUAGGCGCGUGAGCACACUGAA 478
QY 548 GUGGCCUUCGGCGUGGUGGCGCCACUUGCGAGCAGUAGCGCGCAGCAGCAGCAGCAGCAGC 607
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
479 GUGGCCAUUUGGCCUGUGAUUGUGCAACUUGUGAACAGAUUGCUGACUCCGACGCAUCGUCU 538
QY 608 CACAGCGAGAUUGGAGACCAACCAACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 667
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
539 CAUAGGCGAAUUGGUGACACACCAACCCACUAAUACAGACAUAGAGAACAGAAUUGGUUUA 598
QY 668 GCCAGCACCAACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
599 GCCAGCACUACAGCUAAGGCUAUGGAGCAAAUUGGCGUGGAGUAGGAGCAGCAGCAGAG 658
QY 728 GCCAUGGAGGUGGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 787
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
659 GCCAUGGAGGUGUUGAGUCAGGCGUAGGCAAAUUGGCGAAAGCGAGCAAGAGAAACAUUGGAG 718
QY 788 CACCCGAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
719 CAUCCUAGCUCCAGUGCGUGGUCUUGAAAUUGAUUUCUUGAAAUUUGCAGGCGCUAUCAG 778
QY 848 AAGCGCAUGGCGCGUGCAGAUAGCAGCGCUUCAAAGUAAACUAGUGACUUGAAGCGCGUGG 907
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
779 AAACGAAUUGGGGUGGAGAUAGCAACCGUUCAGUGAAACUAGUGACUUGAAGCGCGUGG 838
QY 908 GCUUCCCAACGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 967
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
839 GCUUCCCAACGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 898
QY 968 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1011
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
899 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942
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RESULT 6
US-10-866-484-9
; Sequence 9, Application US/10866484
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```
; Publication No. US20050013826A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, M.
; APPLICANT: Schneider, A.
; TITLE OF INVENTION: Vaccine Compositions and Methods
; FILE REFERENCE: 25955-003CIP
; CURRENT APPLICATION NUMBER: US/10/866,484
; CURRENT FILING DATE: 2004-06-11
; PRIOR APPLICATION NUMBER: 60/435,500
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 10/741,466
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; TYPE: DNA
; LENGTH: 986
; ORGANISM: Influenza A virus
; US-10-866-484-9

Query Match      48.9%; Score 494; DB 8; Length 986;
Best Local Similarity 66.5%; Pred. No. 5.1e-90;
Matches 504; Conservative 89; Mismatches 165; Indels 0; Gaps 0;

Qy 128 AGCCUGUGACCGAGGUGAGACCUACGUGUGAGCAUCAUCCCGAGCGGCCCGCUGAAG 187
Db 4 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTATCGTCCGTCAGGCCCTCAA 63
Qy 188 GCCGAGAUCCGCGAGGUCGAGGACGUGUUGCGCGCAAGAACACCGACUGAGGUG 247
Db 64 GCCGAGATCGCGCGAGACTTGAAGATGTTCTTTGCTGGGAAGAACACCGATCTCGAGGCA 123
Qy 248 CUGAUGGAGUGGUCGAGACGACGACGACCAUCCUGAGCCCGCUGACCAAGGGAUCCUGGCG 307
Db 124 CTCATGGAATGGCTAAGAACAGAACCAATCTCTGACCTGACTAAGGGGATTTTAGGA 183
Qy 308 UUCGUGUACCCUGACCGUGCGCCAGCGCGCGCCUGCAGCGCGCGCGCGUGUGUGAG 367
Db 184 TTTGTGTTACGCTCAGCTGCGTCCAGTGAGCGAGGACTGCGAGCGTTGTCAG 243
Qy 368 AACGCCUUGAACGGCAACCGCGACCCCAACAAUGGACAAAGGCGGUGAAGCUGUACAGG 427
Db 244 AATGCCCTTAATGGGAATGGGGATCCAAACAAATGAGACAGGGGAGTGAACCTGTACAGG 303
Qy 428 AAGCUGAGAGGAGGAUACCUUCCAGCGCGCGCAGGAGUACGCCUGAGCUACAGCGCC 487
Db 304 AAGCTCAAAAGGGAAATTAATTCACCGGGCCAAAGAAAGTAGCGCTCAGTTATTCTACT 363
Qy 488 GCGCGCCUGGCGCAGCUGAUGGCGCGUGAUCUACAAACAGAGUUGGCGCGUGACCAACGAG 547
Db 364 GTGCACTTGCAGCTGATGGGCTCATATACACAGATGGGAGCTGTAAACCACTGAA 423
Qy 548 GUGGCUUUGGCGUGUGUGCGCCACCUUGCGAGCAGAUUGCGCGACAGCCAGCCGAGC 607
Db 424 GTGGCATTGCGCTAGTGTGTGCCACTTGTGAGCAGATTGTCGACTCCCGACATCGGTCC 483
Qy 608 CACAGGAGAUUGUGUACCAACCAACCCUUGAUCAGGACGAGAGAACAGAUUGUGUG 667
Db 484 CACAGACAGATGGTGACGACCAACCAACCACTAATCAGACATGAGAACAGGATGGTG 543
Qy 668 GCCAGCACCGCCGAGGCAUGGAGCAGAUUGGCGCGCGCAGCAGCGAGCGCGCGCGAG 727
Db 544 GCCAGTACCGGCTAAGGCCATGAGCAGATGGCAGGGTTCGATGTGAACAGGAGCAGAA 603
Qy 728 GCCAUGAGGUGGCGCAGCGCAGGCGAGGUGUGCAGGCGCAGGAGCAACUUGGCAACC 787
Db 604 GCCATGAGAGTTGCTAGTCAGGCTAGGCGAGATGGTGCAGGCAATGAGAACCACTTGGGACT 663
Qy 788 CACCCACAGCAGCGCGCGCGUGAAGAAACGACUUGCUGGAGAACCUUGCAGGCUUACAG 847
Db 664 CACCCTAGCTCCAGTGGCGGCTTAAAGATGATCTTCTTGAATAATTTGAGGCCCTTACAG 723
Qy 848 AAGCGCAUGGGCGUGAGCAGGCGCGUACAGUAGAAC 885

; US-10-729-830-1
; Sequence 1, Application US/10729830
; Publication No. US20050032730A1
; GENERAL INFORMATION:
; APPLICANT: Von der Muelbe, Florian
; APPLICANT: Hoerr, Ingmar
; APPLICANT: Pascolo, Steve
; TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
; FILE REFERENCE: 2793-1-001PCT/CIP
; CURRENT APPLICATION NUMBER: US/10/729,830
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: PCT/EP02/06180
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Influenza virus
; FEATURE:
; OTHER INFORMATION: Influenza matrix: wildtype gene (for comparison)
; FEATURE:
; OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
; OTHER INFORMATION: codon: tga (nucleotides 767 to 769)
; US-10-729-830-1

Query Match      48.1%; Score 485.8; DB 8; Length 774;
Best Local Similarity 65.4%; Pred. No. 2.2e-88;
Matches 498; Conservative 91; Mismatches 172; Indels 0; Gaps 0;

Qy 128 AGCCUGUGACCGAGGUGAGACCUACGUGUGAGCAUCAUCCCGAGCGGCCCGCUGAAG 187
Db 14 AGTCTTCTAACCGAGGTCGAAACGTACGTTCTCTATCATCCCGTCAGGCCCTCAA 73
Qy 188 GCCGAGAUCCGCGAGGUCGAGGACGUGUUGCGCGCAAGAACACCGACUGAGGUG 247
Db 74 GCCGAGATCGCAGAGACTTGAAGATGTTCTTTGCGAGGGAAGAACACCGATCTTGAAGTT 133
Qy 248 CUGAUGGAGUGGUCGAGACGAGCCCAUCCUGAGCCCGCUGACCAAGGGAUCCUGGCG 307
Db 134 CTCATGGAATGGCTAAGAACAGAACCAATCTCTGCTCCTGACTAAGGGGATTTTAGGA 193
Qy 308 UUCGUGUACCCUGACCGUGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 367
Db 194 TTTGTGTTACGCTCAGCTCAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 253
Qy 368 AACGCCUUGAACCGCGACCGCGACCCCAACAAUGGACAAAGGCGGUGAAGCUGUACAGG 427
Db 254 AATGCCCTTAATGGGAACCGGGATCCAAATAACATGACAAAGCAGTTAAACTGTATAGG 313
Qy 428 AAGCUGAGAGGAGGAUACCUUCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 487
Db 314 AAGCTCAAGAGGAGGATTAACATTCCATGGGGGCCAAAGAAATCTCAGTATTCTGCT 373
Qy 488 GCGCGCCUGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 547
Db 374 GTTGCACTTGCAGTTGTTATGGGCTCATATACACAGGATGGGGGTGTGACCACTGAA 433
Qy 548 GUGGCUUUGGCGUGUGUGCGCCACCUUGCGAGCAGAUUGCGCGACAGCCAGCACCGGAGC 607
Db 434 GTGGCATTGCGCTAGTGTGTGCCACTTGTGCAACCTGTGAACAGATTCGTACTCCAGCATCGGTCT 493
Qy 608 CACAGGAGAUUGGAGCACCAACCAACCCUUGAUCAGGCGACGAGACAGNAGUUGUGUG 667
Db 494 CATAGGCAATGGTGACAAACCAACCCCACTAATCAGATGAGATGAGAAACAGATGGTTTA 553
Qy 668 GCCAGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 727
```


Db 554 GCCAGCACTACAGCTAAGGCTATGGAGCAATGGCTCGATCGAGTGAGCAAGCAGCAGAG 613
Qy 728 GCAUGAGAGUGGCGACGAGGCGCAGGAGAGUGGUGGAGGCAUGAGGACCAUCGGCACC 787
Db 614 GCCATGAGAGTGTAGTACAGGCTAGGCAATGGTGCAGGGATGAGAACCATTTGGGACT 673
Qy 788 CACCCAGCAGCAGCGCGCCUGAAGAACGACACCGUGGAGAACCCUGCAGGCGCUACCGAG 847
Db 674 CATCTAGCTCCAGTGTGGTCTGAAATAATGATCTTCTTGAAATTTGCGAGGCTATCAG 733
Qy 848 AAGCGCAUGGCGUGCAGAGCAGCGCGUCCAGUACUAG 888
Db 734 AAACGAATGGGGTGCGAGATGCAACCGTTCAAGTGAAC TAG 774

RESULT 8

US-10-177-390-31
; Sequence 31, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Influenza virus
US-10-177-390-31

Query Match 47.6%; Score 481.2; DB 6; Length 1027;
Best Local Similarity 65.3%; Pred. No. 1.9e-87;
Matches 495; Conservative 90; Mismatches 173; Indels 0; Gaps 0;

Qy 128 AGCCUGUGCAGCGAGGUGGAGACCUAGCUGUGAGAGCAUCCCGAGCGGCCCCUGAAG 187
Db 29 AGTCTTCTAACCGAGGTGGAACGTACGTTCTCTATCATCCCGTCAGGCCCCCTCAA 88
Qy 188 GCCGAGAUCCGCCAGAGCUGGAGGACGUGUUCGCCGACAGAACACCGCAGGAGGUG 247
Db 89 GCCGAGATCGCACAGAGACTTGAAGATGCTTTGCGAGGAAGAACACCGATCTTGAGGTT 148
Qy 248 CUGAUGAGUGGUGAAGACAGGCGCCAUCCUGAGCGCCCGCAGCAAGGGAUCCUGGGC 307
Db 149 CTCATGGAATGGCTAAAGACAAGACCAATCTCTGACCTGACTAAGGGGATTTAGGA 208
Qy 308 UUCGUGUACCCUGACCGUGCAGGCGCGCCUGCAGCGCCCGCGCUUCUGUGCAG 367
Db 209 TTTGTGTTCAGCTCACCGTCCAGTGCAGAGACTTGCAGCGTAGACGCTTTGTCCAA 268
Qy 368 AACGCCUUGAACCGGCAACCGCGACCCCAAACAAUGGACAAAGGCGCGUGAAGCUGUACAGG 427
Db 269 AATGCCCTTANTGGNACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTATAGG 328
Qy 428 AAGCUGAAGAGGGAGAUCAUCUCCACGCGCCGCAAGGAGAUACGCGUGACUACAGCGCC 487
Db 329 AAGCTCAAGAGGGAGATAAATTCATGGGGCCAAAGAAATCTCACTCAGTTATTTCTGCT 388
Qy 488 GGCGCCUGGCGACGUGCAGGCGCGUGAUCAACACAGAGUUGGCGCGUGACCAACCGAG 547
Db 389 GGTGCACTTGCGCAGTTGTATGGGCTCATATACAAAGATGGGGGCTGTGACCACTGTAA 448
Qy 548 GUGGCGCUUCGCGUGGUGGCGCCACCGCAGCAGAGUUCGCGCGCAGCAGCAGCGCAGC 607
Db 449 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCACGATCGGTCT 508
Qy 608 CACAGGCAGAGUGGUGACCAACCAACCCUUCAGUACAGGCGACGAGAACAGGAUGGUGUG 667

Db 509 CATAGGCAAAATGGTGAACAACCAACCAACCACTAATCAGACATGAGAACAGATGGTTTA 568
Qy 668 GCCAGCACCAACCGCCCAAGCGCAUGGAGCAGAUUGCGCGGAGCAGCAGCAGCGCGCAG 727
Db 569 GCCAGCACTACAGCTAAGGCTATGGAGCAAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG 628
Qy 728 GCAUGAGAGUGGCGCAGCGCAGGCGCAGGAGUGGUGGAGGAGGAGGAGGAGGAGGAGGAGG 787
Db 629 GCCATGAGGTTGCTAGTACAGGCTAGGCAATGGTGCAGGATGAGAACCAATTTGGGACT 688
Qy 788 CACCCAGCAGCAGCGCGCCUGAAGAACGACACCGUGGAGAACCCUGCAGGCGCUACCGAG 847
Db 689 CATCTAGCTCCAGTGTGGTCTGAAATAATGATCTTCTTGAAATTTGCGAGGCTATCAG 748
Qy 848 AAGCGCAUGGCGUGCAGAGCAGCGCUCCAGUACUAG 885
Db 749 AAACGAATGGGGTGCGAGATGCAACCGTTCAAGTGATC 786

RESULT 9

US-10-855-875-5
; Sequence 5, Application US/10855875
; Publication No. US20050003349A1
; GENERAL INFORMATION:
; APPLICANT: Kawaoka, Yoshihiro
; TITLE OF INVENTION: High Titer Recombinant Influenza Viruses for Vaccines and Gene
; FILE REFERENCE: 800.038US1
; CURRENT APPLICATION NUMBER: US/10/855,875
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: US 60/473,798
; PRIOR FILING DATE: 2003-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Influenza virus
US-10-855-875-5

Query Match 47.4%; Score 479.6; DB 8; Length 1027;
Best Local Similarity 64.6%; Pred. No. 4.1e-87;
Matches 495; Conservative 92; Mismatches 179; Indels 0; Gaps 0;

Qy 128 AGCCUGUGACCGCAGGUGGAGACCUAGCUGUGAGCAUCCCGAGCGGCCCCUGAAG 187
Db 29 AGTCTTCTAACCGAGGTGCAAAACGTACTCTCTATCATCCCGTCAGGCCCCCTCAA 88
Qy 188 GCCGAGAUCCGCCAGAGGCGUGGAGGAGCUGUUCGCCGCAAGAACACCGCAGGAGGUG 247
Db 89 GCCGAGATCGCACAGAGACTTGAAGATGCTTTTGCAGGGAAGAACACCGATCTTGAGGTT 148
Qy 248 CUGAUGAGUGGUGGAGAGACAGGCGCCCAUCCUGAGCGCCCGCAGCAAGGGAUCCUGGGC 307
Db 149 CTCATGGAATGGCTAAAGACAAGACCAATCTCTGACCTCTGACTAAGGGGATTTAGGA 208
Qy 308 UUCGUGUACCCUGACCGUGCAGGCGCGCCUGCAGCGCGCCCGCGCUUCUGUGCAG 367
Db 209 TTTGTGTTCAGCTCACCGTCCAGTGCAGGAGGACTTGCAGCGTAGACGCTTTGTCCAA 268
Qy 368 AAGCCUUGAACCGGCAACCGCGACCCCAAACAAUGGAGAACGCGCGUGAAGCUGUACAGG 427
Db 269 AATGCCCTTAAATGGGAACCGGGATCCAAATAACATGGACAAAGCAGTTAACTGTATAGG 328
Qy 428 AAGCUGAAGAGGGAGAUCAUCUCCAGCGCGCCCAAGGAGAUACGCGUGACUACAGCGCC 487
Db 329 AAGCTCAAGAGGGAGATAAATTCATGGGGCCAAAGAAATCTCACTCAGTTATTTCTGCT 388
Qy 488 GGCGCCUGGCGCAGCUGCAGUUGGCGCGUACUACAAAGGAGUUGGCGCGCGCAGCAGCGAG 547
Db 389 GGTGCACTTGCGCAGTTGTATGGGCTCATATACAAAGATGGGGGCTGTGACCACTGTAA 448
Qy 548 GUGGCGCUUCGCGUGGUGGCGCCACCGCAGCAGAGUUCGCGCGCAGCAGCAGCGCAGC 607


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Db 449 GTGGCATTTGGCCTGGTATGTGCAACCTGTGAAACAGATTGCTGACTCCAGCATCGGTCT 508
Qy 608 CACAGGAGAGUGGUGACACACCAACCCUGAUCAGGACGAGAACAGAGUUGUCUG 667
Db 509 CATAGGCAATGGTGACAAACCAATCCACTAATCAGATGAGAACAGAAATGGTTTAA 568
Qy 668 GCCAGCACCAACCGCCAAAGGCCAUGAGAGCAGAUUGGCCGCGCAGCAGCGAGCGCCGAG 727
Db 569 GCCAGCACTACAGCTAAGGCTATGGAGCAATGCTGGATCGAGTGAAGCAGCAGAG 628
Qy 728 GCCAUGAGAGUGGCGCAGCGCCAGCAGAGUUGGUGAGGCGCAUAGAGAACUUGCGCAC 787
Db 629 GCCATGGAGGTGTAGTCAGGCTAGACAAATGCTGCAAGCGATGAGAACCAATTGGGACT 688
Qy 788 CACCCAGCAGCAGCGCGCCUGAAGAACGACCUUGUGGAGAACUUGCAGGCGCUACCGAG 847
Db 689 CATCTAGCTCCAGTGTGCTGAAATATGATCTTCTGAAATTTGCGAGGCTATCAG 748
Qy 848 AAGCGCAUGGCGUGCAGAGCAGCGCUUACAAGUAAACUAGUGACU 893
Db 749 AAACGAATGGGGTGCAGATGCAACGGTTCAGGTGATCCTCTCACT 794
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RESULT 10

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US-10-065-133A-1
; Sequence 1, Application US/10065133A
; Publication No. US20030195074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (673)..(673)
; OTHER INFORMATION: At nucleotide 673, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-065-133A-1
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```
Query Match 47.2%; Score 477.6; DB 6; Length 1023;
Best Local Similarity 65.0%; Pred. No. le-86;
Matches 493; Conservative 90; Mismatches 175; Indels 0; Gaps 0;

Qy 128 AGCCUGCUGACCGAGGUGGAGACUACGUGCUGAGCAUCAUCCAGCGGCCCGCCUGAAG 187
Db 28 AGTCTTCTGACCGAGGTGCAACGATGCTCTCTATCTATCATCAGGCCCGCCCTCAA 87
Qy 188 GCCGAGAUCCGCCAGGCGUGGAGGACGUGUUGCCGCGGCAAGAACACCGACCUUGAGGUG 247
Db 88 GCCGAGATCGCGCAGAGACTTGAAGATGTCTTTGACGGGAGAACACCGATCTTGAGGCA 147
Qy 248 CUGAUGAGUGGUGUAGAGACAGCGCCCAUCCUGAGGCCUUGACCAAGGCGAUCCUGGGC 307
Db 148 CTCATGGAATGGCTAAAGACCAAGACCAATCTGTCACTCTGTACTTAAGGGATTTAGGA 207
Qy 308 UUCGUGUACCCUGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 367
```

```
Db 208 TTGCTATTACGCTCACCGTGCAGTGCAGGAGACTGCAGCGGTAGACGCTTTGTCCAA 267
Qy 368 AAGCCCUAGAACGGCAACGGCAGCCCAACAAUAGGACAGCCCGUGAAGCUGUACAGG 427
Db 268 AATGCCCTTATGTGGAACCGGAGATCCAAACAAATGACAGAGCAGTAAACTGTACAGG 327
Qy 428 AAGCUGAAGAGGAGAUACCUUCCAGCGCGCCAAAGAGAGAUACGCCUUGAGCUACAGGCGC 487
Db 328 AAGCTTAAAGAGAAATAACATTCCATGGGGGAAAAGAGGTGGCACTCAGCTATTCCACT 387
Qy 488 GGGCCCUUGGCCAGCAGCUGCAGUUGGCGCUGAUCUACAACAGAUUGGCGCGGUGACCAACCGAG 547
Db 388 GGTGCACTAGCCAGCTGCTGGACTCATATACAAACAGAAATGGGAACTGTGACAAACGAA 447
Qy 548 GUGGCCUUGCGCGCUGGUGCGCACCUUGCGAGCAGAUCCGCCAGCAGCAGCAGCGGAGC 607
Db 448 GTGGCATTTGGCCCTGCTGATGCGCCACATGTGAACAGATCGCTGATTTCCAGCATCTCAT 507
Qy 608 CACAGGAGAGUGGUGACCAACCAACCCCGCCUGAUCAGGCGCACGAGAACAGAGUUGUCUG 667
Db 508 CACAGGAGATGTGACAAACCAACCCATTAAATCAGACATGAAACAGAAATGTTATTA 567
Qy 668 GCCAGCACCAACCGCCAAAGGCCAUGGAGCAGAUUGCGCGGCGAGCGCAGCGCGCGAG 727
Db 568 GCCAGTACCAACGGCTAAAGCCATGGAGCAGATGGCAGGGTCCGAGTGAGCAGGCGAGCAG 627
Qy 728 GCCAUGAGGUGGCCAGCGCCAGGCGCAGCAGUUGGUGGCGCAGGAGCAUUGCGGACCC 787
Db 628 GCCATGGAGGTTCGTAGTAGGCTAGGCTAGGCTGTCAGGCAATGAGAACCAATTTGGGACC 687
Qy 788 CACCCAGCAGCAGCGCGCCUGAAGAACGACCUUGCUGGAGAACCUUGCAGGCGCUACCGAG 847
Db 688 CACCTAGCTCCAGTGGCGGTTTGAAGATGATCTCTCTGAAATTTGCGAGGCGCTACAG 747
Qy 848 AAGCGCAUGGCGUGCAGAGUUGCAGCGCUUACAAGUAAAC 885
Db 748 AAACGGATGGGAGTGCAAAATGCAGCGATTCAAGTGATC 785
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RESULT 11

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US-10-434-811A-1
; Sequence 1, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (663)..(663)
; OTHER INFORMATION: At nucleotide 663, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-434-811A-1
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RESULT 13
US-10-872-014-1
; Sequence 1, Application US/10872014
; Publication No. US20040234553A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher Edu
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT FILING DATE: 2004-06-18
; PRIOR FILING DATE: 2003-05-08
; PRIOR FILING DATE: 2003-05-08
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 1999-08-12
; PRIOR FILING DATE: 1999-08-12
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(780)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (663)..(663)
; OTHER INFORMATION: At nucleotide 663, r = a or g
; OTHER INFORMATION: At amino acid residue 213, Xaa = Val
US-10-872-014-1
Query Match 47.2%; Score 477.6; DB 8; Length 1023;
Best Local Similarity 65.0%; Pred. No. 1le-86;
Matches 493; Conservative 90; Mismatches 175; Indels 0; Gaps 0;
Qy 128 AGCCUGUGACCGGAGGAGACCUACGUGUGAGCAUCCUCCAGCGGCGCCUUAAG 187
Db AGCTTCTGACCGAGGTGGAACGTCAGTCTCTCTATCTGTCATCATGAGCCCTCAA 87
Qy 188 GCCGAGUCCGCCAGCGGAGGAGCGUGUUCGCCGCAAGAACACCGACCGUGAGGUG 247
Db GCCGAGATCGGCGAGAGACTTGAAGATGCTTTTGCAGGGAAGAACCGATCTTTGAGCA 147
Qy 248 CUGAGGAGUGGUGAAGACAGCGCCCAUCCUGAGCGCCUUGACCAAGGCAUCCUGGC 307
Db CTCATGGAATGGCTAAAGACAGAACCAATCTGTCACCTCTGACTAAAGGATTTAGGA 207
Qy 308 UUCGUGUACCCUGACCGUGCGGAGCGGCGGCGUGUCCGCGCAAGAACCGUGGAG 367
Db TTGATTCAGCTCACCGTCCCGAGTGAGGAGAGCTGCGAGCTGAGCGTTGTCAA 267
Qy 368 AACGCCUUGAACCGGCAACCGGCGCCCAACAAUGGACAGGCGGUGAAGCUGUACAGG 427
Db AATGCCCTTAGTGGAAACGGAGATCCAAACAAATGACAGAGCAGTAAACCTGACAGG 327
Qy 428 AAGCUGAAGAGGGAUACCUUCCAGCGCGCCCAAGAGAGUACGCUUGAGCUACAGGCC 487
Db AAGCTTAAAGAGAAATAACATTCATCGGGGCAAAAGAGGTGGCACTCATGTTTCACT 387
Qy 488 GGCGCCUGGCGAGCGGCGUGAUCUACACAGAGUGGCGCGGUGACCCAGG 547
Db GTGCACTAGCAGCTGATGGGACTCATATACACAGATGGGAACCTGTGACAAACGAA 447
Qy 548 GUGCGCUUGCGGUGUGGCCCAUCCUGGAGCAGAUCCGCCAGACAGCAGCACCGCAGC 607
Db GTGCACTTGGCTTGGTATGGCCCAACATGTGAACAGATCGTGTATCCAGCATCGATCT 507
Qy 608 CACAGGAGAGUGGUGACCAACCAACCCUUGAUCAGGACGAGAACAGAGUGGUGUG 667
Db CACAGGAGAGTGGTGACCAACCAACCCATTATATCATGATGAAACAGAGTGTATTA 567
Qy 668 GCCAGCACACCGCCCAAGGCGCAUGGAGCAGGCGGCGGAGCAGGAGGCGCGCGAG 727
Db GCCAGTACCAACCGCTAAAGCGCATGGAGCAGATGCGAGGGTCTGAGTGAGCAGGAG 627
Qy 728 GCCAUGGAGUGGCGCAGGCGCAGGCGCAGGAGGCGGCGGAGGAGGAGGAGGAGG 787
Db GCCATGGAGGTTGCTAGTAAGGCTAGGCGATGTRCAGGCAATGAGAACCTTTGGGAGC 687
Qy 788 CACCCAGCAGCAGCGCGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 847
Db CACCTAGCTCCAGTGCCGGTTTGAAAGATGATCTCTTGAATAATTTGCGAGGCTACCA 687
Qy 848 AAGCGCAUGGCGGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 885
Db AAACGGATGGGAGTGCAATATGCAAGGATTCAGAGTGATC 785
RESULT 14
US-10-371-525-13
; Sequence 13, Application US/10371525
; Publication No. US20030203869A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.01
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 1999-05-13
; PRIOR FILING DATE: 1999-05-13
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PADRE-Influenza matrix construct encoding fusion
; OTHER INFORMATION: of pan DR epitope sequence to amino-terminus of
; OTHER INFORMATION: influenza matrix protein gene
; NAME/KEY: CDS
; LOCATION: (16)...(816)
; OTHER INFORMATION: PADRE-Influenza matrix
US-10-371-525-13
Query Match 47.2%; Score 477.4; DB 6; Length 816;
Best Local Similarity 64.4%; Pred. No. 1le-86;
Matches 504; Conservative 88; Mismatches 191; Indels 0; Gaps 0;
Qy 101 GCCUGGCCUAGCCACCGAGCCUGGCGGCGGAGCCUGAGCCAGGUGGAGACCUACGUGCUG 160
Db GCCTGGACCTGAAGGCTGCGCTATGAGTCTTTAAACCGAGGTGCGAAACGTACGTTCTC 93
Qy 161 AGCAUACUCCCGAGCGGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGAGGAGG 220
Db TCTATCATCCCATCAGCGGCGGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGAGG 153
Qy 221 GCCGCGAAGAACACCGAGGAGGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGAG 280
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Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues
Total number of hits satisfying chosen parameters: 16046624

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	730.6	72.3	756	12	US-11-131-479-27
2	686.8	67.9	759	12	US-11-131-479-69
3	686.8	67.9	1050	12	US-11-131-479-59
4	665.4	65.8	982	12	US-11-131-479-61
5	664.8	65.8	759	12	US-11-131-479-79
6	594.6	58.8	756	12	US-11-131-479-26
7	488	48.3	756	12	US-11-131-479-3
8	476.4	47.1	1027	12	US-11-131-479-3
9	473	46.8	1305	12	US-11-131-479-45
10	460.4	45.5	987	12	US-11-155-478A-131
11	454	44.9	982	12	US-11-131-479-60
12	454	44.9	4822	12	US-11-131-479-95
13	454	44.9	5161	12	US-11-131-479-101
14	454	44.9	5398	12	US-11-131-479-91
15	454	44.9	7798	12	US-11-131-479-97
16	454	44.9	7798	12	US-11-131-479-98
17	454	44.9	7798	12	US-11-131-479-99
18	454	44.9	7798	12	US-11-131-479-100
19	454	44.9	8442	12	US-11-131-479-106
20	454	44.9	8442	12	US-11-131-479-107

21	454	44.9	8450	12	US-11-131-479-104	Sequence 104, App
22	454	44.9	8450	12	US-11-131-479-105	Sequence 105, App
23	447.6	44.3	1027	12	US-11-155-478A-130	Sequence 130, App
24	401.8	39.7	629	9	US-11-137-807-18	Sequence 18, Appl
25	77.4	7.7	1180	12	US-11-116-746-2	Sequence 2, Appl
26	77.4	7.7	1180	12	US-11-116-746-4	Sequence 4, Appl
27	75.8	7.5	588	12	US-11-136-527-1488	Sequence 1488, Ap
28	75.8	7.5	588	12	US-11-136-527-5584	Sequence 5584, Ap
29	75.2	7.5	1677	7	US-10-515-547-3	Sequence 3, Appl
30	75.2	7.4	4339	8	US-10-909-125-801	Sequence 801, App
31	74.8	7.4	2475	9	US-11-197-133A-17	Sequence 17, Appl
32	74.8	7.4	5152	8	US-10-240-708-47	Sequence 47, Appl
33	74.6	7.4	1395	8	US-10-955-054A-111	Sequence 111, App
34	74.6	7.4	2217	7	US-10-947-249-197	Sequence 197, App
35	74.6	7.4	3819	8	US-10-973-115B-405	Sequence 405, App
36	74.6	7.4	3819	8	US-10-131-826A-405	Sequence 405, App
37	74.4	7.4	600	12	US-11-136-527-6371	Sequence 6371, Ap
38	74.4	7.4	2020	12	US-11-090-617-697	Sequence 697, App
39	74.4	7.4	2430	7	US-10-649-457-3	Sequence 3, Appl
40	74.4	7.4	3015	12	US-11-183-136-39	Sequence 39, Appl
41	74.4	7.4	4409	12	US-11-136-527-2275	Sequence 2275, Ap
42	74.2	7.3	1905	8	US-10-947-249-132	Sequence 132, App
43	74	7.3	1690	12	US-11-090-439-43	Sequence 43, Appl
44	73.8	7.3	588	8	US-10-689-742-41	Sequence 41, Appl
45	73.6	7.3	762	9	US-11-096-568A-1243	Sequence 1243, A

ALIGNMENTS

RESULT 1
US-11-131-479-27
; Sequence 27, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein
US-11-131-479-27

Query Match	72.3%	Score	730.6	DB	12	Length	756
Best local Similarity	86.3%	Pred. No.	3.5e-77				
Matches	650	Conservative	89	Mismatches	14	Indels	0
Gaps	0						
Qy	128	AGCCUGCAGACCCGAGGUGGAGACCUACGUGUGAGCAUCCAGCCAGCGGCCCCUGAAG	187				
Db	4	AGCCTGCTGACCGAGGTGGAGACCTACGCTGTGAGCATATCCCGCGGCCCTTGAGG	63				
Qy	188	GCCGAGAUCCGCCAGAGCGUGGAGGACGUGUUCGCCGCAAGAACACCCAGCUGGAGGUG	247				
Db	64	GCCGAGATGCCACAGAGGCTGGAGGACGTGTTCGCCGCAAGAACACCCAGCCTGAGGTG	123				
Qy	248	CUGAUGAGUGGUCUGAAGACAGCGCCCAUCCUGAGCCCCUGACCAAGGGAUCCUGGCG	307				
Db	124	CTGATGGATGGCTGAAGACAGCGCCCATCTGTAGGCCCTCTGACCAAGGGCATCTCTGGGC	183				


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; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Open Reading Frame for the M2M1 Fusion from VR4755
US-11-131-479-59

Query Match      67.9%; Score 686.8; DB 12; Length 1050;
Best Local Similarity 82.6%; Pred. No. 4,1e-72;
Matches 623; Conservative 89; Mismatches 42; Indels 0; Gaps 0;

QY 130 CCUGCUGACCGAGGUGGAGACCUACGUCUGAGCAUCAUCCCGAGCGGCCCGCCUAGAGGC 189
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
297 CTTGCTTGACAGAAAGTGAAGCAATACGCTGAGCATCGTCCAGCGCGGCCCGCCCTGAAGGC 356
QY 190 CGAGAUCCGCCAGAGCGUGGAGGACGUGUUGCGCGCAAGAACACCGACCUUGGAGGUGCU 249
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
357 CGAGATCGCCCNAGACACTGGAGGAGCTGTTGCCCGCAAGAACACCGACCTGGAGGCCCT 416
QY 250 GAUGGAGUGGUGAAGACACAGGCCCAUCCUGAGCGCCCGUAGACCAAGGCAUCCUGGGCUU 309
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
417 GATGAGTGGCTGAAGACACAGACCCATCTGAGCGCCCTGACCAAGGCGCATCTGGGCTT 476
QY 310 CGUGUUCACCCUGACCGUGGCCAGCGAGCGCGCGGCGUGCAGCGCGCGCGCGCGCGCGCG 369
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
477 CGTGTTCACCTGACCGTGCCTGCGAGAGAGGCTGCGAGAGAAAGATTCTGTCAGAA 536
QY 370 CGCCUGAAGCGCAACCGCGACCCCAACAAUGGACAAAGCGCGUGAAGCUGUACAGAA 429
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
537 CGCCTTGAAAGCGGAAACGGGAGCCCAACATGACCGCGCGCGCTGAAGCTGTACCGGAA 596
QY 430 GUGAAGAGGAGAUCAUCCUUCACGGCGCAAGGAGAUCAAGCTGAGCUACAGCGCGG 489
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
597 GCTGAAGAGAGAGATCACTTCCACGGCGCAAGGAGATCGCCTGAGCTACAGCGCGG 656
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DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
657 CGCCTGGCCAGCTGCATGGGCTGATCTACACAGAAATGGGCGCGCTGACACCGAGGT 716
QY 550 GGCUUCGCGCUGUGUGCGCACCTGCGAGCAGAUCCGACAGCGCGCGCGCGCGCGCGCGCG 609
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
717 GGCCTTGGCTGTGTGGCCACCTGCGAGAGATCGCCACAGCGCGCGCGCGCGCGCGCGCG 776
QY 610 CAGGAGAGUGGACCAACCAACCCCGUAGCAGGCAACAGGAAACAGGAGUGGUGCGG 669
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
777 CAGACAGATGTGGCCACCAACCAACCCCGTATCAGACACAGAAACAGAAATGGTGTGGC 836
QY 670 CAGACACCGCCAAAGGCGUAGAGCAGAUUGGCGCGAGCAGCGCGCGCGCGCGCGCGCG 729
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837 CAGCACCAACCCCAAGGCGATGAGAGCAGATGGCGCGCGAGCAGCGAGCGCGCGCGAGGC 896
QY 730 CAUGGAGUGGCGCAGCGCGCGCGCGAGAGUGGCGCGCGCGCGCGCGCGCGCGCGCGCG 789
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
897 CATGAGATCGCCAGCGCGCGCGCGAGAGATGGTGGAGGCCATGAGAGCCATCGGACCCCA 956
QY 790 CCCAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 849
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
957 CCCAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1016
QY 850 GCGAUGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 883
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1017 GAGAATGGGCGTGCAGATGCAGAGATTCAAGTGA 1050
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RESULT 4

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US-11-131-479-61
; Sequence 61, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
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; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 982
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Codon Optimized Segment 7 from VR4763
US-11-131-479-61
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Query Match      65.8%; Score 665.4; DB 12; Length 982;
Best Local Similarity 80.2%; Pred. No. 1.3e-69;
Matches 612; Conservative 90; Mismatches 61; Indels 0; Gaps 0;

QY 128 AGCCUGCUGACCGAGGUGGAGACCUACGUCUGAGCAUCAUCCCGAGCGGCCCGCCUAGAG 187
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 AGCCTGCTGACCGAGGTGCAAAACGATGTTCTCTATCGTGGCGCGGCCCGCCCTGAAG 63
QY 188 GCCGAGAUCCGCCAGGCGUGGAGGACGUGUUGCGCGCAAGAACACCGACCUUGGAGGUG 247
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 248 CUGAUGGAGUGGUGAAGACACAGGCCCAUCCUGAGCGCCCGUAGACCAAGGCAUCCUGGGC 307
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124 CTGATGAGTGGCTGAAGACACAGACCCATCTGAGCGCCCTGACCAAGGCGCATCTGGGC 183
QY 308 UUCGUGUACCCUGACCGUGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
184 TTGCTGTTCACCTGACCGTGCCTGCGAGGAGGCGCTGCAGAGAAAGATTCTGTGCGAG 243
QY 368 AACGCCUGAAGCGCAACCGCGACCCCAACAAUGGACAAAGCGCGUGAAGCUGUACAGG 427
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244 AACGCCCTGAAACGGCAACGGCGAGCCCAACATGACAGAGCGCTGTGAGCTGTACAGA 303
QY 428 AAGCUGAAGAGGAGAUCAUCCUUCACGGCGCGCAAGGAGAUCAUCCUGAGCUACAGCGCC 487
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
304 AAGCTGAAGAGAGAGATCACTTCCACGGCGCGCAAGGAGATCGCCTGAGCTACAGCGCC 363
QY 488 GCGCGCCUGGCGAGCUGCAUGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 547
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
364 GCGCGCCUGGCGAGCTGCTGATGGGCTGATCTACACAGAAATGGGCGCGCTGACACCGAG 423
QY 548 GUGGCCUUCGCGCUGUGUGCGCACCTGCGAGCAGAUCCGCGACAGCGCGCGCGCGCGCG 607
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
424 GTGGCTTCGCGCTGTGTGTGCGCACCTGCGAGCAGATCGCCGACAGCGCGCGCGCGCGAG 483
QY 608 CACAGGAGAGUGGAGUACACACCAACCCCGUAGCAGGCAACGAGAAACAGGAGUGGUGUG 667
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
484 CACAGACAGATGTGGCCACCAACCAACCCCTGATCAGACACGAGAACAGAAATGGTGTG 543
QY 668 GCGACACACCGCGCAAGGCGCAUGGAGCAGAUUGGCGCGCGAGCGAGCGAGCGCGCGCG 727
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
544 GCCAGCACCAACCGCGCAAGGCGCATGGAGCAGATGGCGCGCGAGCGAGCGAGCGCGCGAG 603
QY 728 GCCAUGGAGUGGCGCAGCGCGCGCGCGAGCGAGUGGCGCGCGCGCGCGCGCGCGCGCG 787
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
604 GCCATGGAGATCGCCAGCGCGCGCGAGCGAGATGTGTGCGAGCGCGCGCGCGCGCGCGCG 663
QY 788 CACCCAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
664 CACCCAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 723
QY 848 AAGCGCAUGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 890
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
724 AAACGAATGGGGGTGCAGATGCACAGATTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 766
```

```
RESULT 5
US-11-131-479-79
; Sequence 79, Application US/111311479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 79
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Optimized M1 Coding Region
US-11-131-479-79

Query Match      65.8%; Score 664.8; DB 12; Length 759;
Best Local Similarity 80.7%; Pred. No. 1.6e-69;
Matches 610; Conservative 89; Mismatches 57; Indels 0; Gaps 0;

Qy      128 AGCCUGUGUACCGGAGGUGGAGACCUAGCGUGUGAGCAUCAUCCCGGCGGCCCGCCUGAAG 187
Db      4 AGCTGTGCTGACCGAGGTGCGAACGATGTTCTCTATGTCGCCAGCGGCCCGCTGAAG 63

Qy      188 GCCGAGAUCCGCGAGCGUGGAGGACCGUUGUUCGCGCGCAAGAACACCGACCGUGGUG 247
Db      64 GCCGAGATCGCCAGACTGGAGGACGTGTTCGCGCGCAAGAACACCGACCTGGAGGCC 123

Qy      248 CUGAUGGAGUGGUGUAGACGACCGACCCCAUCCUGAGCCCGCCUGACCAAGGGCAUCCUGGCC 307
Db      124 CTGATGGAGTGGCTGAAGACAGACCCATCTCTGAGCCCGCTGACACAGGGGATCTCTGGCC 183

Qy      308 UUCGUGUUCACCCUGACCGUGCCCGAGGCGCGCCUGCAGCGCCCGCGCGUUGUGUAG 367
Db      184 TTCGTGTTACCTTGACCGTGCACGCGAGAGAGCGCTGCAGAGAGAGAAAGATTGCTGCAG 243

Qy      368 AACGCCUGAACGGCAACGGCGACCCCAACCAUGGACCAAGGAGUACGUCUGAGCUACAGCGCC 427
Db      244 AACGCCCTGAACGGCAACGGCGACCCCAACCAATGGAAGAGCGGTGAAGCTGTACAGA 303

Qy      428 AAGCUGAAGAGGAGUACCUUCCAGCGCGCAAGGAGUACAGCGCGCGUGAAGCUGUACAGG 487
Db      304 AAGCTGATTAACACTGACCGTGCCTCCGAGAGAGCGCTGCAGCGGAGAGGTTGCTTCAG 243

Qy      488 GCGCGCCUGGCGAGCUGCAUGGCGCGUGAUCAACAGGAUGGGCGCGCGUACCAACCGAG 547
Db      364 GCGCGCTTGGCGCTGATGCGGCTGATCTACACAGAAATGGCGCGCGTGAACCAACCGAG 423

Qy      548 GUGGCUUUGGCGUGGUGGCGCCACCGUGGAGCAGAUCCGCGAGCAGUCCGCGAGCAGCGCAGC 607
Db      424 GTGGCTTTCGGCTGGTGGCGCACCTCGCAGCAGATCGCGCAGCAGCGACGACGACAGAAAGC 483

Qy      608 CACAGGAGAGUGGUGUACCAACCAACCCUGAUCAGGCAAGGAGCAGGAGAGGUGUGUG 667
Db      484 CACAGACAGATGGTGGCGCACCAACCAACCCCTGATCAGACAGAGACAGATGGTGTG 543

Qy      668 GCCAGCACACCGCCCAAGGCCAUGGAGCAGAUUGGCGCGCAGCAGCAGCGCCCGAG 727
Db      544 GCCAGCACCAACCGCCCAAGGCCATGGAGCAGATGGCGCGCAGCAGCGAGCGCGCCGAG 603

Qy      728 GCCAUGGAGGUGGCCAGCGCCAGGCGAGGUGGUGAGGCGGCGGAGGAGGAGGAGGAGGAGG 787
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Db      604 GCCATGGAGATGCCAGCCAGCCAGACAGATGGTGCAGGCGCATGAGAGCCATCGGCACC 663

Qy      788 CACCCCGAGCAGCAGCGCCCGCGUGAAGACGACCGUUGAGAGCAGCGUGGAGAACCGUGAGCCUACAG 847
Db      664 CACCCCGAGCAGCAGCGCCCGCTGAAAGATGATCTTCTTGAATAATTGCAGACCTATCAG 723

Qy      848 AAGCGCAUGGGCGUGCAGGAUGCAGCGCUUCAAGUGA 883
Db      724 AACGAATGGGGTGCAGATGCAACGATTCAAGTGA 759

RESULT 6
US-11-131-479-28
; Sequence 28, Application US/111311479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131.479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 28
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human Codon Optimized Influenza A Virus M1 Protein
US-11-131-479-28

Query Match      58.8%; Score 594.6; DB 12; Length 756;
Best Local Similarity 75.0%; Pred. No. 2.2e-61;
Matches 565; Conservative 89; Mismatches 99; Indels 0; Gaps 0;

Qy      128 AGCCUGUGACCGGAGGUGGAGACCUAGCGUGUGAGCAUCAUCCCGGCGGCCCGCCUGAAG 187
Db      4 AGTCTGCTGACAGAGGTTGAGACGTGCTGTCCATCATTCCTCAGGCCCGCCCTGAAG 63

Qy      188 GCCGAGAUCCCGAGCGUGGAGGACCGUUGUUCGCGCGCAAGAACACCGACCGUGAGGUG 247
Db      64 GCCGAGATTGCCAGAGACTGGAGAGGTCTTCGCCGCGCAAGAACACCGATCTGGAGGTG 123

Qy      248 CUGAUGGAGUGGUGAAGACGACCGCCCAUCCUGAGCCCGCCUGACCAAGGCGAUCCUGGCC 307
Db      124 CTGATGGAGTGGCTGAAGACTCGCCCCATCTCTCTCCCTGACAAAGGCGATCCTGGGC 183

Qy      308 UUCGUGUUCACCCUGACCGUGCCCGAGGCGCGCGCGUGCAGCGCCCGCGCGUUGUGUAG 367
Db      184 TTCGTATTAACACTGACCGTGCCTCCGAGAGAGCGCTGCAGCGGAGAGGTTGCTTCAG 243

Qy      368 AACGCCUGAACGGCAACGGCGACCCCAACCAUGGACCAAGGAGUACAGCGCGUGAAGCUGUACAGG 427
Db      244 AACGCCCTGAACGGCAACGGCGATCCCAACCAATGGAAGAGCGGTGAAGCTGTATAGA 303

Qy      428 AAGCUGAAGAGGAGUACCUUCCAGCGCGCAAGGAGUACAGCGCGCGUGAAGCAGCGCC 487
Db      304 AAGCTGAAAGCAGAGATCACATTTTCATGGCGCCCAAGGAGATATCGCTGAGCTACAGTGCC 363

Qy      488 GCGCGCCUGGCGAGCUGCAUGGCGCGUGAUCAACAGGAUGGGCGCGCGUACCAACCGAG 547
Db      364 GCGCGCTTGGCGCTGATGCGGCTGATCTACACAGAAATGGCGCGCGTGAACCAACCGAG 423

Qy      548 GUGGCUUUGGCGUGGUGGCGCCACCGUGGAGCAGAUCCGCGAGCAGUCCGCGAGCAGCGCAGC 607
Db      424 GTGGCTTTCGGCTGGTGGCGCACCTCGCAGCAGATCGCGCAGCAGCGACGACGACAGAAAGC 483

Qy      608 CACAGGAGAGUGGUGUACCAACCAACCCUGAUCAGGCAAGGAGCAGGAGAGGUGUGUG 667
Db      484 CACAGACAGATGGTGGCGCACCAACCAACCCCTGATCAGACAGAGACAGATGGTGTG 543

Qy      668 GCCAGCACACCGCCCAAGGCCAUGGAGCAGAUUGGCGCGCAGCAGCAGCGCCCGAG 727
Db      544 GCCAGCACCAACCGCCCAAGGCCATGGAGCAGATGGCGCGCAGCAGCGAGCGCGCCGAG 603

Qy      728 GCCAUGGAGGUGGCCAGCGCCAGGCGAGGUGGUGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGG 787
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149	CTCTGGAATGGCTAAAGACAAGACCAATCTCTGCTACCTCTGACTAAGGGGATTTTATAGA	208
Qy	UUCUGUUCUACCCUGACCGUGCCACGAGAGCGCGCCUCGAGCGCGCCGCUUCUGUCAG	367
Db	TTTGTGTTCAAGCTCACCCTGCGCCAGTCGAGCGAGGACTGCGAGGTAGAGCGCTTTGTCCAA	268
Qy	AAGCGCCUGAAACGGCAACGGCGACCCCAACAAACGACAAGGCCUGUAGAAGUCAGG	427
Db	AATGCCCTTTAATGGGAAACGGGGATCCAAATTAACATGGACAAGACGACTTAACCTGTATAGG	328
Qy	AAGCUGAAGAGGAGGAUACACCUUCCACGCGCCCAAGGAGAUACGACGUCACUACAGCGCC	487
Db	AAGCTCAAGAGGGAGATACATCTTCATGGGGCCAAAGAAATCTCAGTTCAGTTATTCGTCT	388
Qy	GGCGCCCGUGCCAGCUGCAUGGGCCUGUAUCACCAACAGGAUGGGCGCGUGACCAACCGAG	547
Db	GGTGCACTTTGCCAGTTGATGGCGCTCATATACAACAGGATGGGGCTGTGACCACTGAAC	448
Qy	GUGGCCUUCGCGCGUGUGCGCCACUUGCGAGCAGCAUGCCGACAGCAGCAGCAGCCGAGC	607
Db	GTGGCAATTTTGGGCTGGTATGTGTGCAACCTGTGTGAACAGATTTGCTATCCCAAGCATCGGTCT	508
Qy	CACAGSCAUAUGUGUACACCAACCAACCCCUUGAUCAGGCACAGAAACAGAUUGUGUCUG	667
Db	CATAGGCAAAATGGTGACAAACACCAATCCACTATTCAGACATGAGAAACAGAAATGGTTTTA	568
Qy	GCAGACCAACCGCCAAAGGCCAUGGACAGAUGGCCGCGACAGCAGCAGCGCGCCGAG	727
Db	GCCAGCACTACAGCTAAGGCTATGGAGCAAAATGGCTGGATCGAGTGAGCAAGCAGCAGAG	628
Qy	GCCAUGGAGGCGCCAGCCAGGCGCAGAGUUGUGCAGGCGCAUGAGGACCAUUGCGACC	787
Db	GCCATGGAGGTTTGCTAGTCAGGCTTAGACAAATGGTGCAAGCGATGAGAAACCATTTGGGACT	688
Qy	CACCCAGCAGCAGCGCGCCUGAAGAACGACCUUGUGGAGAACCUUGCAGGCCUACCCAG	847
Db	CATCTTAGCTCCAGTGCTGGTCTGAAAATATGATCTTTGAAAATTTTGCAGGGCTATCAG	748
Qy	AAGCGCAUGGGCGUGCAGAUAGCAGCGCCUUCAAAGUGAAC	885
Db	AAACGAATGGGGTGCAGATGCAACGGTTTCAAGTGATC	786

RESULT 9

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US-11-131-479-45
; Sequence 45, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 1305
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Influenza A Virus M1 Fused to Synthetic HbcAg
US-11-131-479-45

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Query Match      46.8%; Score 473; DB 12; Length 1305;
Best Local Similarity 64.9%; Pred. No. 2.8e-47;
Matches 489; Conservative 89; Mismatches 175; Indels 0; Gaps 0;
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PRECIPITATION 10

```

RES001 10
US-11-155-478A-131
; Sequence 131, Application US/11155478A
; Publication No. US20060014140A1
; GENERAL INFORMATION:
;
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE LAVAL
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING RESPIRATORY VIRUSES
; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; CURRENT FILING DATE: 2005-06-20
; PRIORITY APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 174

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Db	664	CATCTAGTCCAGTGGTCTAAAGATGATCTTCTTGAATAATTTGCAGACCTATCAG	723
Qy	848	AAGCGCAUGGGCGGCGCAGNUGCAGCGCTUUCAGUGAAC	885
Db	724	AAACGAATGGGGGTGCAGATGCAACGATTCAGGTGACC	761

RESULT 12
US-11-131-479-95
; Sequence 95, Application US/11131479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530, 0640002/EJH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95
; LENGTH: 4822
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4764, Ligation of VR4756 RV-Sali into VR10682 RV
; US-11-131-479-95

1297	CATAGC	AAATGGT	GCACAC	CAACCA	ATCCATTA	ATAAGGCAT	GAGACAG	AAGTGT	TTTG	1356				
668	GCCAG	CACCA	CCGCC	CAAGGCC	CAUGG	CAGCAG	AUGGCCG	CAGCAG	CAGCGCCG	CAG	727			
1357	GCCAG	CACCTAC	AGCTA	AGGCTAT	TGGAG	CAAAATGGCT	TGGATCA	AGTGAG	CAGCAGCG	CAG	1416			
728	GCCAU	GAGG	UGGCC	CAGCC	CAGG	CAGAG	UGGCG	CAGCC	CAUGAGG	ACCAU	CGG	787		
1417	GCCAT	GGAAT	TCTAGT	CAGGC	CCAGC	CAAAATGGT	GCAGG	CAATG	AGCCAT	TGGG	ACT	1476		
788	CACCC	CAGC	AGC	CGCCG	CCUGA	AGAAC	CGAC	CUCG	CUGG	AGAAC	CUCG	CAG	847	
1477	CATCT	TAGT	CCAGT	GCTGGT	CTA	AAAGAT	GTATCT	TCTTG	GA	AAATTTG	CAGAC	CTAT	CAG	1536
848	AAGCG	CAUGGG	CGUG	CAG	AUGC	AGCG	CAGC	CGCU	CAUG	AAC	885			
1537	AAACGA	ATGGGGT	GCAGAT	GC	AACG	ATTC	CAAGT	CAAGT	GACC	1574				

```

RESULT 13
US-11-131-479-101
; Sequence 101, Application US/11131479
; Publication No. US2006024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vilalta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EUH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 101
; LENGTH: 5161
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR4770, M2 Insert Replacing WNV Insert in VR6430
US-11-131-479-101

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[illegible]

[illegible]

Search completed: March 21, 2006, 01:31:39
Job time : 461.616 secs